

SCORE Search Results Details for Application 09556178 and Search Result 20101214_103254_us-09-556-178-3.rag.

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This page gives you Search Results detail for the Application 09556178 and Search Result 20101214_103254_us-09-556-178-3.rag.

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GenCore version 6.3
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OM protein - protein search, using sw model

Run on: December 14, 2010, 11:22:17 ; Search time 40 Seconds
(without alignments)
5898.160 Million cell updates/sec

Title: US-09-556-178-3
Perfect score: 994
Sequence: 1 MKIWTSEHVFDHPWETVTTA.....TASARGTIRTPMAAAFAEK 194

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 6395994 seqs, 1224146475 residues

Total number of hits satisfying chosen parameters: 6395994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_201023:*
1: geneseq1:*
2: geneseq2:*
3: geneseq3:*

SUMMARIES

Result No.	Score	% Query Match	Length	DB ID	Description
1	994	100.0	194	1 AAY49959	Aay49959 Human ves
2	994	100.0	194	1 AAB03814	Aab03814 Human ves
3	994	100.0	194	1 AAB93664	Aab93664 Human pro
4	994	100.0	194	2 AJL92872	Ajl92872 Human tis
5	981	98.7	211	1 ADN05056	Adn05056 Antipsori
6	981	98.7	211	1 ADP55417	Adp55417 Human PRO
7	981	98.7	211	2 AJL92871	Ajl92871 Human tis
8	892	89.7	268	2 AJL92348	Ajl92348 Human tis
9	820	82.5	164	1 ABP69539	Abp69539 Human pol
10	653	65.7	172	1 ADA54780	Ada54780 Human pro
11	584	58.8	143	1 ABO57277	Abo57277 Human gen
12	524	52.7	215	1 ABB64259	Abb64259 Drosophil
13	524	52.7	215	2 AFB99526	Afb99526 Fruit fly
14	524	52.7	215	3 AXY18738	Axy18738 Drosophil

15	524	52.7	228	3	AXY18708	Axy18708	Bombyx mo
16	522	52.5	231	3	AXY18712	Axy18712	Nasonia v
17	521	52.4	223	3	AXY18736	Axy18736	Tribolium
18	501	50.4	225	3	AXY18714	Axy18714	Aedes aeg
19	437	44.0	243	3	AXY18718	Axy18718	Culex qui
20	321	32.3	59	1	AAG02195	Aag02195	Human sec
21	281.5	28.3	194	3	AXX92111	Axx92111	High yiel
22	281.5	28.3	194	3	AXY18734	Axy18734	Candida a
23	281.5	28.3	235	3	AXY18726	Axy18726	Kluyverom
24	280	28.2	184	3	AXX92105	Axx92105	High yiel
25	280	28.2	184	3	AXY18730	Axy18730	Yarrowia
26	275	27.7	184	3	AXX92083	Axx92083	High yiel
27	275	27.7	184	3	AXY18710	Axy18710	Schizosac
28	273.5	27.5	215	3	AXY18728	Axy18728	Debaryomy
29	270	27.2	230	3	AXY18706	Axy18706	Saccharom
30	263	26.5	183	1	AAG17835	Aag17835	Arabidops
31	263	26.5	183	1	ADT55760	Adt55760	Plant pol
32	263	26.5	183	2	ALJ51753	Alj51753	Plant pro
33	263	26.5	183	2	AXE54591	Axe54591	Hexadecad
34	263	26.5	183	2	ARM28857	Arm28857	Arabidops
35	263	26.5	183	2	ARM73343	Arm73343	Arabidops
36	263	26.5	183	2	ARM32447	Arm32447	Arabidops
37	263	26.5	183	3	AUR38505	Aur38505	Arabidops
38	263	26.5	183	3	AXX92081	Axx92081	High yiel
39	263	26.5	222	1	AAG17834	Aag17834	Arabidops
40	263	26.5	222	2	ALJ51752	Alj51752	Plant pro
41	263	26.5	222	2	ARM32446	Arm32446	Arabidops
42	263	26.5	222	2	ARM73342	Arm73342	Arabidops
43	263	26.5	222	2	ARM28856	Arm28856	Arabidops
44	257.5	25.9	224	2	AXE54607	Axe54607	Hexadecad
45	257.5	25.9	224	3	AXY18724	Axy18724	Candida g

ALIGNMENTS

RESULT 1

AA49959

ID AA49959 standard; protein; 194 AA.

XX

AC AA49959;

XX

DT 15-JUN-2007 (revised)

DT 04-FEB-2000 (first entry)

XX

DE Human vesicle trafficking protein 2.

XX

KW Human; vesicle trafficking protein; VTP-1; VTP-2; VTP-3; apoptosis;

KW cancer; inflammation; BOND_PC; CGI-107 protein;

KW CGI-107 protein [Homo sapiens]; C20orf45; dJ543J19.5;

KW hypothetical protein LOC51012;

KW hypothetical protein LOC51012 [Homo sapiens]; SLMO2; slowmo homolog 2;

KW slowmo homolog 2 [Homo sapiens]; PRELID3B;

KW chromosome 20 open reading frame 45, isoform CRA_a;

KW chromosome 20 open reading frame 45, isoform CRA_a [Homo sapiens];

KW chromosome 20 open reading frame 45;

KW chromosome 20 open reading frame 45 [Homo sapiens];

KW slowmo homolog 2 (Drosophila);

KW Slowmo homolog 2 (Drosophila) [Homo sapiens]; unnamed protein product;

KW unnamed protein product [Homo sapiens]; G05215; G05488; G07283; G08345.

XX

OS Homo sapiens.

XX

PN US5989859-A.

XX

PD 23-NOV-1999.

XX

PF 07-NOV-1997; 97US-00967364.
 XX
 PR 07-NOV-1997; 97US-00967364.
 XX
 PA (INCY-) INCYTE PHARM INC.
 XX
 PI Bandman O, Guegler KJ, Corley NC, Lal P, Shah P;
 XX
 DR WPI; 2000-022782/02.
 DR N-PSDB; AAZ35834.
 DR PC:NCBI; gi117553615.
 DR PC:SWISSPROT; Q9Y3B1.
 XX
 PT Novel vesicle trafficking proteins used in the diagnosis, prevention, and
 PT treatment of inflammation or cancer.
 XX
 PS Claim 9; Fig 4; 55pp; English.
 XX
 CC The present sequence represents the human vesicle trafficking protein
 CC designated VTP-2. VTPs can be used in a method for preventing or treating
 CC disease associated with an increase in apoptosis. The method can treat
 CC diseases such as cancer and inflammation, by administering a VTP
 CC antagonist
 CC
 CC Revised record issued on 15-JUN-2007 : Enhanced with precomputed
 CC information from BOND.
 XX
 SQ Sequence 194 AA;

Query Match 100.0%; Score 994; DB 1; Length 194;
 Best Local Similarity 100.0%;
 Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKIINTSEHVFDPWETVTTAAMQKYPNPMNPVSVGVDDLRHIDPSGKLHSHRLLSTEWG 60
 Db 1 MKIINTSEHVFDPWETVTTAAMQKYPNPMNPVSVGVDDLRHIDPSGKLHSHRLLSTEWG 60
 Qy 61 LPSIVKSLIGAARTKTYVQEHSVVDPVEKTMELKSTNISFTNMVSDERLIYKPHPQDPE 120
 Db 61 LPSIVKSLIGAARTKTYVQEHSVVDPVEKTMELKSTNISFTNMVSDERLIYKPHPQDPE 120
 Qy 121 KTVLTQEAIIITVKGVSLSYLEGLMASTISSNASKGREAMEWVHKLNABIEELTASARG 180
 Db 121 KTVLTQEAIIITVKGVSLSYLEGLMASTISSNASKGREAMEWVHKLNABIEELTASARG 180
 Qy 181 TIRTPMAAAFAEK 194
 Db 181 TIRTPMAAAFAEK 194

RESULT 2
 AAB03814

ID AAB03814 standard; protein; 194 AA.

XX
 AC AAB03814;
 XX
 DT 15-JUN-2007 (revised)
 DT 13-OCT-2000 (first entry)
 XX
 DE Human vesicle trafficking protein-2 (VTP-2) amino acid sequence.
 XX
 KW Vesicle trafficking protein; VTP-2; human; cancer; inflammation; asthma;
 KW foetal development; Crohn's disease; diabetes; multiple sclerosis;
 KW rheumatoid arthritis; infection; ulcerative colitis; proliferation;
 KW irritable bowel syndrome; apoptosis; AIDS; Alzheimer's disease;
 KW Parkinson's disease; osteoporosis; wasting disorder; BOND_PC;
 KW CGI-107 protein; CGI-107 protein [Homo sapiens]; C20orf45; dJ543J19.5;

KW hypothetical protein LOC51012;
 KW hypothetical protein LOC51012 [Homo sapiens]; SLMO2; slowmo homolog 2;
 KW slowmo homolog 2 [Homo sapiens]; PRELID3B;
 KW chromosome 20 open reading frame 45, isoform CRA_a;
 KW chromosome 20 open reading frame 45, isoform CRA_a [Homo sapiens];
 KW chromosome 20 open reading frame 45;
 KW chromosome 20 open reading frame 45 [Homo sapiens];
 KW slowmo homolog 2 (Drosophila);
 KW Slowmo homolog 2 (Drosophila) [Homo sapiens]; unnamed protein product;
 KW unnamed protein product [Homo sapiens]; G05215; G05488; G07283; G08345.

XX
 OS Homo sapiens.
 XX
 KN US6071703-A.
 XX
 PD 06-JUN-2000.
 XX
 PF 04-AUG-1999; 99US-00368408.
 XX
 PR 07-NOV-1997; 97US-00967364.
 XX
 PA (INCY-) INCYTE PHARM INC.
 XX
 PI Guegler KJ, Shah P, Corley NC, Bandman O, Lal P;
 XX
 DR WPI; 2000-422079/36.
 DR N-PSDB; AAA59874.
 DR PC:NCBI; g1117553615.
 DR PC:SWISSPROT; Q9Y3B1.

XX
 PT Identifying polynucleotides encoding vesicle trafficking proteins (VTP)
 PT for treating and preventing e.g. inflammation, by detecting a
 PT hybridization complex of a nucleic acid from a sample and a
 PT polynucleotide encoding a VTP.

XX
 PS Claim 1; Fig 4; 55pp; English.

XX
 CC This sequence represents human vesicle trafficking protein (VTP-2) amino
 CC acid sequence. VTP-2 encoding cDNA was isolated from a bronchial
 CC epithelium cell line cDNA library (BEPINOT01). VTP-2 has structural and
 CC chemical homology with an avian homologue of assembly protein (AP) small
 CC chains, pX19. The present invention relates to a method for detecting
 CC human VTP encoding polynucleotide sequences and includes nucleotide and
 CC protein sequences for human VTP-1, VTP-2 and VTP-3. Northern analysis of
 CC VTP-1, 2, and 3 shows that their expression is associated with cancer,
 CC inflammation and foetal/infant development. The method of the invention
 CC is useful for screening and identifying a polynucleotide encoding a human
 CC VTP, which may be used for the diagnosis, prevention, or treatment of
 CC inflammation associated disorder, e.g. asthma, Crohn's disease, diabetes,
 CC multiple sclerosis, rheumatoid arthritis, infections, ulcerative colitis
 CC and irritable bowel syndrome. Other diseases and disorders identified,
 CC prevented or treated with polynucleotide sequences encoding VTP include
 CC those associated with cell proliferation or apoptosis, such as AIDS,
 CC Alzheimer's disease, Parkinson's disease, osteoporosis, wasting diseases
 CC and cancer

CC
 CC Revised record issued on 15-JUN-2007 : Enhanced with precomputed
 CC information from BOND.

XX
 SQ Sequence 194 AA;

Query Match 100.0%; Score 994; DB 1; Length 194;
 Best Local Similarity 100.0%;
 Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKIWTSEHVFDPHWETVTTAAMQKYPNPNMNSVVGVDVLRHDIPSGKLHSHRLLSTEWG 60
 |||

```

Db          1 MKIWTSEHVFDPHWETVTTAAMQKYPNPMNPSVVGVDVDRHIDPSGKLHSHRLLSTEWG 60
Qy          61 LPSIVKSLIGAARTKTYVQEHSVVDPVEKTMELKSTNISFTNMVSVDERLIYKPHPQDPE 120
            |||
Db          61 LPSIVKSLIGAARTKTYVQEHSVVDPVEKTMELKSTNISFTNMVSVDERLIYKPHPQDPE 120
            |||
Qy          121 KTVLTQEAIIITVKGVSLSYLEGLMASTISSNASKGREAMEWVVIHKLNAEIEELTASARG 180
            |||
Db          121 KTVLTQEAIIITVKGVSLSYLEGLMASTISSNASKGREAMEWVVIHKLNAEIEELTASARG 180
            |||
Qy          181 TIRTPMAAAFAEK 194
            |||
Db          181 TIRTPMAAAFAEK 194
            |||

```

RESULT 3

AAB93664

ID AAB93664 standard; protein; 194 AA.

XX

AC AAB93664;

XX

DT 15-JUN-2007 (revised)

DT 26-JUN-2001 (first entry)

XX

DE Human protein sequence SEQ ID NO:13188.

XX

KW Human; primer; detection; diagnosis; antisense therapy; gene therapy;

KW BOND_PC; CGI-107 protein; CGI-107 protein [Homo sapiens]; C20orf45;

KW dJ543J19.5; hypothetical protein LOC51012;

KW hypothetical protein LOC51012 [Homo sapiens]; SLMO2; slowmo homolog 2;

KW slowmo homolog 2 [Homo sapiens]; PRELID3B;

KW chromosome 20 open reading frame 45, isoform CRA_a;

KW chromosome 20 open reading frame 45, isoform CRA_a [Homo sapiens];

KW chromosome 20 open reading frame 45;

KW chromosome 20 open reading frame 45 [Homo sapiens];

KW slowmo homolog 2 (Drosophila);

KW Slowmo homolog 2 (Drosophila) [Homo sapiens]; unnamed protein product;

KW unnamed protein product [Homo sapiens]; GO5215; GO5488; GO7283; GO8345.

XX

OS Homo sapiens.

XX

PN EP1074617-A2.

XX

PD 07-FEB-2001.

XX

PF 28-JUL-2000; 2000EP-00116126.

XX

PR 29-JUL-1999; 99JP-00248036.

PR 27-AUG-1999; 99JP-00300253.

PR 11-JAN-2000; 2000JP-00118776.

PR 02-MAY-2000; 2000JP-00183767.

PR 09-JUN-2000; 2000JP-00241899.

XX

PA (HELI-) HELIX RES INST.

PA (REAS-) RES ASSOC FOR BIOTECHNOLOGY.

XX

PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;

PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;

XX

DR WPI; 2001-318749/34.

DR PC:NCBI; gill17553615.

DR PC:SWISSPROT; Q9Y3B1.

XX

PT Primer sets for synthesizing polynucleotides, particularly the 5602 full-

PT length cDNAs defined in the specification, and for the detection and/or

PT diagnosis of the abnormality of the proteins encoded by the full-length

PT cDNAs.

XX
 PS Claim 8; SEQ ID NO 13188; 2537pp + Sequence Listing; English.
 XX
 CC The present invention describes primer sets for synthesising 5602 full-
 CC length cDNAs defined in the specification. Where a primer set comprises:
 CC (a) an oligo-dT primer and an oligonucleotide complementary to the
 CC complementary strand of a polynucleotide which comprises one of the 5602
 CC nucleotide sequences defined in the specification, where the
 CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
 CC of an oligonucleotide comprising a sequence complementary to the
 CC complementary strand of a polynucleotide which comprises a 5'-end
 CC sequence and an oligonucleotide comprising a sequence complementary to a
 CC polynucleotide which comprises a 3'-end sequence, where the
 CC oligonucleotide comprises at least 15 nucleotides and the combination of
 CC the 5'-end sequence/3'-end sequence is selected from those defined in the
 CC specification. The primer sets can be used in antisense therapy and in
 CC gene therapy. The primers are useful for synthesising polynucleotides,
 CC particularly full-length cDNAs. The primers are also useful for the
 CC detection and/or diagnosis of the abnormality of the proteins encoded by
 CC the full-length cDNAs. The primers allow obtaining of the full-length
 CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
 CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893
 CC represent human amino acid sequences; and AAH13629 to AAH13632 represent
 CC oligonucleotides, all of which are used in the exemplification of the
 CC present invention
 CC
 CC Revised record issued on 15-JUN-2007 : Enhanced with precomputed
 CC information from BOND.
 XX
 SQ Sequence 194 AA;

Query Match 100.0%; Score 994; DB 1; Length 194;
 Best Local Similarity 100.0%;
 Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKIWTSEHVDFHPWETVTTAAMQKYPNPMNPSVVGVDVLDLRHIDPSGKLHSHRLLSTEWG 60
 Db 1 MKIWTSEHVDFHPWETVTTAAMQKYPNPMNPSVVGVDVLDLRHIDPSGKLHSHRLLSTEWG 60
 Qy 61 LPSIVKSLIGAARTKTYVQEHSVVDPVEKTMELKSTNISFTNMVSVDERLIYKPHQDPE 120
 Db 61 LPSIVKSLIGAARTKTYVQEHSVVDPVEKTMELKSTNISFTNMVSVDERLIYKPHQDPE 120
 Qy 121 KTVLTQEAIIITVKGVSLSSYLEGLMASTISSNASKGREAMEWVIHKLNAEIELTASARG 180
 Db 121 KTVLTQEAIIITVKGVSLSSYLEGLMASTISSNASKGREAMEWVIHKLNAEIELTASARG 180
 Qy 181 TIRTPMAAAFAEK 194
 Db 181 TIRTPMAAAFAEK 194

RESULT 4

AJL92872

ID AJL92872 standard; protein; 194 AA.

XX

AC AJL92872;

XX

DT 24-JAN-2008 (first entry)

XX

DE Human tissue-derived serum glycoprotein SEQ ID NO:8527.

XX

KW Diagnostic; protein detection; mass spectroscopy; glycoprotein;
 KW biomarker; prostate tumor; breast tumor; liver tumor; bladder tumor;
 KW prostatitis; benign prostatic hyperplasia.

XX

OS Homo sapiens.

XX
PN WO2007047796-A2.
XX
PD 26-APR-2007.
XX
PF 17-OCT-2006; 2006WO-US040784.
XX
PR 17-OCT-2005; 2005US-0728044P.
XX
PA (SYST-) INST SYSTEMS BIOLOGY.
XX
PI Zhang H, Aebersold RH;
XX
DR WPI; 2007-560359/54.
XX
PT New diagnostic panel comprising detection reagents that are specific for
PT tissue-derived serum glycoprotein, useful in defining a disease-
PT associated tissue-derived blood fingerprint or monitoring response to
PT therapy in a subject.
XX
PS Disclosure; SEQ ID NO 8527; 242pp; English.
XX
CC The invention relates to a new diagnostic panel comprising detection
CC reagents, where each detection reagent is specific for one tissue-derived
CC serum glycoprotein, where the glycoproteins detected are derived from the
CC same tissue. The invention also relates to a method for defining a
CC biological state of a subject, a method for defining a disease-associated
CC tissue-derived blood fingerprint, a method for detecting perturbation of
CC a normal biological state in a subject, a method for monitoring a
CC response to a therapy in a subject, a targeting agent comprising a tissue
CC -derived probe that specifically recognizes a sequence, where the probe
CC has attached a therapeutic agent comprising a radioisotope or cytotoxic
CC agent, and an assay device comprising a panel of detection reagents where
CC each detection reagent in the panel, with the exception of a negative and
CC positive control, is capable of specific interaction with one of tissue-
CC derived serum glycoproteins present in blood, where the tissue-derived
CC serum glycoproteins are derived from the same tissue and where the
CC pattern of interaction between the detection reagents and the tissue-
CC derived serum glycoproteins present in a blood sample is indicative of a
CC biological condition. The diagnostic panel further comprises one or more
CC detection reagents that are each specific for a prostate-, bladder-,
CC liver-, breast-, lymphocyte- or ovary-derived glycoprotein. The disease
CC is prostate cancer, breast cancer, liver cancer or bladder cancer. The
CC prostate disease is prostate cancer, prostatitis or benign prostatic
CC hyperplasia. The diagnostic panel is useful in defining a disease-
CC associated tissue-derived blood fingerprint, detecting perturbation of a
CC normal biological state in a subject or monitoring a response to a
CC therapy in a subject. This sequence represents a human tissue-derived
CC serum glycoprotein used in the scope of the invention.
XX
SQ Sequence 194 AA;

Query Match 100.0%; Score 994; DB 2; Length 194;
Best Local Similarity 100.0%;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MKIWTSEHVDFHPWETVTTAAMQKYPNPMNPSVVGVDVDRHIDPSGKLHSHRLLSTEWG	60
Db	1	MKIWTSEHVDFHPWETVTTAAMQKYPNPMNPSVVGVDVDRHIDPSGKLHSHRLLSTEWG	60
Qy	61	LPSIVKSLIGAARTKTYVQEHSSVVDPEKTMELKSTNISFTNMVSVDERLIYKPHQDPE	120
Db	61	LPSIVKSLIGAARTKTYVQEHSSVVDPEKTMELKSTNISFTNMVSVDERLIYKPHQDPE	120
Qy	121	KTVLTQEAIIIVKGVSLSSYLEGLMASTISSNASKGREAMEWVIHKLNAEIELTASARG	180
Db	121	KTVLTQEAIIIVKGVSLSSYLEGLMASTISSNASKGREAMEWVIHKLNAEIELTASARG	180

Qy 181 TIRTPMAAAFAEK 194
 |||||||||||||
 Db 181 TIRTPMAAAFAEK 194

RESULT 5

ADN05056

ID ADN05056 standard; protein; 211 AA.

XX

AC ADN05056;

XX

DT 01-JUL-2004 (first entry)

XX

DE Antipsoriatic protein sequence #707.

XX

KW antipsoriatic; gene therapy; psoriasis; diagnosis.

XX

OS Homo sapiens.

XX

PN WO2004028479-A2.

XX

PD 08-APR-2004.

XX

PF 25-SEP-2003; 2003WO-US030907.

XX

PR 25-SEP-2002; 2002US-0414006P.

XX

PA (GETH) GENENTECH INC.

XX

PI Bodary S, Clark H, Jackman J, Schoenfeld J, Williams PM, Wood WI;

PI

XX

DR WPI; 2004-305105/28.

DR

N-PSDB; ADN05055.

XX

PT New PRO nucleic acid or polypeptide, useful for preparing a

PT pharmaceutical composition for diagnosing or treating psoriasis in a

PT

XX

PS Claim 9; SEQ ID NO 1450; 3069pp; English.

XX

CC The invention relates to novel polynucleotide and polypeptides for
 CC treating psoriasis or a sequence having at least 80% identity to the
 CC above sequences. The nucleic acid is useful for preparing a composition
 CC for diagnosing or treating psoriasis in a mammal. This sequence
 CC corresponds to one of the polypeptides of the invention.

XX

SQ Sequence 211 AA;

Query Match 98.7%; Score 981; DB 1; Length 211;

Best Local Similarity 98.5%;

Matches 191; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MKIINTSEHVFDHPWETVTTAAMQKYPNPMNPSVVGVDVDRHIDPSGKLHSHRLLSTEWG 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1 MKIINTSEHVFDHPWETVTTAAMQKYPNPMNPSVVGVDVDRHIDPSGKLHSHRLLSTEWG 60

Qy 61 LPSIVKSLIGAARTKTYVQEHSSVVDPEKTMELKSTNISFTNMVSVDERLIYKPHPQDPE 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 61 LPSIVKSLIGAARTKTYVQEHSSVVDPEKTMELKSTNISFTNMVSVDERLIYKPHPQDPE 120

Qy 121 KTVLTQEAIIITVKGVSLSYLEGLMASTISSNASKGREAMEWVIHKLNAEIELTASARG 180
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 121 KTVLTQEAIIITVKGVSLSYLEGLMASTISSNASKGREAMEWVIHKLNAEIELTASARG 180

Qy 181 TIRTPMAAAFAEK 194

Db 181 TIRTPMAAAAFCRE 194

RESULT 6

ADP55417

ID ADP55417 standard; protein; 211 AA.

XX

AC ADP55417;

XX

DT 15-JUN-2007 (revised)

DT 18-NOV-2004 (first entry)

XX

DE Human PRO protein sequence SEQ ID NO:1393.

XX

KW human; PRO; immune related disease; inflammatory immune response;

KW immune response stimulation; antiallergic; antianaemic; antiarthritic;

KW antiasthmatic; antidiabetic; antiinflammatory; antipsoriatic;

KW antirheumatic; antithyroid; CNS; dermatological; gastrointestinal;

KW haemostatic; hepatotropic; immunostimulant; immunosuppressive; muscular;

KW nephrotropic; neuroprotective; osteopathic; respiratory; vasotropic;

KW virucide; gene therapy; BOND_PC; CGI-107 protein;

KW CGI-107 protein [Homo sapiens]; G05215; G05488; G07283; G08345.

XX

OS Homo sapiens.

XX

PN WO2004039956-A2.

XX

PD 13-MAY-2004.

XX

PF 28-OCT-2003; 2003WO-US034381.

XX

PR 29-OCT-2002; 2002US-0422472P.

XX

PA (GETH) GENENTECH INC.

XX

PI Aggarwal S, Clark H, Gurney AL, Schoenfeld J, Williams PM;

PI Wood WI, Wu TD;

XX

DR WPI; 2004-376182/35.

DR N-PSDB; ADP55416.

DR PC:NCBI; g14929683.

DR PC:SWISSPROT; Q9Y3B1.

XX

PT New PRO polynucleotides and polypeptides, useful in useful in diagnosing

PT and treating an immune related disease, e.g. systemic lupus

PT erythematosus, rheumatoid arthritis, diabetes mellitus or asthma and in

PT stimulating an immune response.

XX

PS Claim 1; SEQ ID NO 1393; 3009pp; English.

XX

CC The present invention describes an isolated PRO nucleic acid (I). Also

CC described: (1) a vector comprising (I); (2) a host cell comprising the

CC vector of (1); (3) a process for producing a PRO polypeptides; (4) an

CC isolated PRO polypeptide; (5) a chimeric molecule comprising the

CC polypeptide of (4) fused to a heterologous amino acid sequence; (6) an

CC antibody which specifically binds to a polypeptide of (4); (7) a

CC composition of matter comprising a polypeptide of (4), an agonist or

CC antagonist of the polypeptide or an antibody that binds to the

CC polypeptide in combination with a carrier; (8) an article of manufacture

CC comprising a container, a label on the container and a composition of

CC matter of (7); (9) a method of treating an immune related disease in a

CC mammal; (10) a method for determining the presence of a PRO polypeptide

CC in a sample suspected of having the polypeptide; (11) a method of

CC diagnosing an immune related disease or an inflammatory immune response

CC in mammal; (12) a method of identifying a compound that inhibits or

CC mimics the activity of or expression of a gene encoding a PRO polypeptide

CC ; and (13) a method of stimulating the immune response in a mammal. The
 CC PRO sequences have antiallergic, antianaemic, antiarthritic,
 CC antiasthmatic, antidiabetic, antiinflammatory, antipsoriatic,
 CC antirheumatic, antithyroid, CNS, dermatological, gastrointestinal,
 CC haemostatic, hepatotropic, immunostimulant, immunosuppressive, muscular,
 CC nephrotropic, neuroprotective, osteopathic, respiratory, vasotropic and
 CC virucide activities, and can be used in gene therapy. The nucleic acid
 CC (I) and the encoded polypeptides, compositions, kits and methods are
 CC useful in diagnosing and treating an immune related disease and in
 CC stimulating an immune response. The present sequence represents a human
 CC PRO protein from the present invention.

CC
 CC Revised record issued on 15-JUN-2007 : Enhanced with precomputed
 CC information from BOND.

XX
 SQ Sequence 211 AA;

Query Match 98.7%; Score 981; DB 1; Length 211;
 Best Local Similarity 98.5%;
 Matches 191; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy	1	MKIWTSEHVFDPHWETVTTAAMQKYPNPNPNSVVGVDVDRHIDPSGKLHSHRLLSTEWG	60
Db	1	MKIWTSEHVFDPHWETVTTAAMQKYPNPNPNSVVGVDVDRHIDPSGKLHSHRLLSTEWG	60
Qy	61	LPSIVKSLIGAARTKTYVQEHSVVDPVEKTMELKSTNISFTNMVSVDERLIYKPHQDPE	120
Db	61	LPSIVKSLIGAARTKTYVQEHSVVDPVEKTMELKSTNISFTNMVSVDERLIYKPHQDPE	120
Qy	121	KTVLTQEAIIITVKGVSLSSYLEGLMASTISSNASKGREAMEWVIHKLNAEIEELTASARG	180
Db	121	KTVLTQEAIIITVKGVSLSSYLEGLMASTISSNASKGREAMEWVIHKLNAEIEELTASARG	180
Qy	181	TIRTPMAAAFAEK	194
Db	181	TIRTPMAAAAFCE	194

RESULT 7

AJL92871

ID AJL92871 standard; protein; 211 AA.

XX

AC AJL92871;

XX

DT 24-JAN-2008 (first entry)

XX

DE Human tissue-derived serum glycoprotein SEQ ID NO:8526.

XX

KW Diagnostic; protein detection; mass spectroscopy; glycoprotein;

KW biomarker; prostate tumor; breast tumor; liver tumor; bladder tumor;

KW prostatitis; benign prostatic hyperplasia.

XX

OS Homo sapiens.

XX

PN WO2007047796-A2.

XX

PD 26-APR-2007.

XX

PF 17-OCT-2006; 2006WO-US040784.

XX

PR 17-OCT-2005; 2005US-0728044P.

XX

PA (SYST-) INST SYSTEMS BIOLOGY.

XX

PI Zhang H, Aebersold RH;

XX

DR WPI; 2007-560359/54.

XX
PT New diagnostic panel comprising detection reagents that are specific for
PT tissue-derived serum glycoprotein, useful in defining a disease-
PT associated tissue-derived blood fingerprint or monitoring response to
PT therapy in a subject.
XX
PS Disclosure; SEQ ID NO 8526; 242pp; English.
XX
CC The invention relates to a new diagnostic panel comprising detection
CC reagents, where each detection reagent is specific for one tissue-derived
CC serum glycoprotein, where the glycoproteins detected are derived from the
CC same tissue. The invention also relates to a method for defining a
CC biological state of a subject, a method for defining a disease-associated
CC tissue-derived blood fingerprint, a method for detecting perturbation of
CC a normal biological state in a subject, a method for monitoring a
CC response to a therapy in a subject, a targeting agent comprising a tissue
CC -derived probe that specifically recognizes a sequence, where the probe
CC has attached a therapeutic agent comprising a radioisotope or cytotoxic
CC agent, and an assay device comprising a panel of detection reagents where
CC each detection reagent in the panel, with the exception of a negative and
CC positive control, is capable of specific interaction with one of tissue-
CC derived serum glycoproteins present in blood, where the tissue-derived
CC serum glycoproteins are derived from the same tissue and where the
CC pattern of interaction between the detection reagents and the tissue-
CC derived serum glycoproteins present in a blood sample is indicative of a
CC biological condition. The diagnostic panel further comprises one or more
CC detection reagents that are each specific for a prostate-, bladder-,
CC liver-, breast-, lymphocyte- or ovary-derived glycoprotein. The disease
CC is prostate cancer, breast cancer, liver cancer or bladder cancer. The
CC prostate disease is prostate cancer, prostatitis or benign prostatic
CC hyperplasia. The diagnostic panel is useful in defining a disease-
CC associated tissue-derived blood fingerprint, detecting perturbation of a
CC normal biological state in a subject or monitoring a response to a
CC therapy in a subject. This sequence represents a human tissue-derived
CC serum glycoprotein used in the scope of the invention.
XX
SQ Sequence 211 AA;

Query Match 98.7%; Score 981; DB 2; Length 211;
Best Local Similarity 98.5%;
Matches 191; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy	1	MKIWTSEHVDFHPWETVTTAAMQKYPNPMNPSVVGVDVDRHIDPSGKLHSHRLLSTEWG	60
Db	1	MKIWTSEHVDFHPWETVTTAAMQKYPNPMNPSVVGVDVDRHIDPSGKLHSHRLLSTEWG	60
Qy	61	LPSIVKSLIGAARTKTYVQEHSVVDPVEKTMELKSTNISFTNMVSVDERLIYKPHQDPE	120
Db	61	LPSIVKSLIGAARTKTYVQEHSVVDPVEKTMELKSTNISFTNMVSVDERLIYKPHQDPE	120
Qy	121	KTVLTQEAIIITVKGVSLSYLEGLMASTISSNASKGREAMEWVIHKLNAEIELTASARG	180
Db	121	KTVLTQEAIIITVKGVSLSYLEGLMASTISSNASKGREAMEWVIHKLNAEIELTASARG	180
Qy	181	TIRTPMAAAFAEK	194
Db	181	TIRTPMAAAFAEK	194

RESULT 8
AJL92348
ID AJL92348 standard; protein; 268 AA.
XX
AC AJL92348;
XX
DT 24-JAN-2008 (first entry)
XX

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This page gives you Search Results detail for the Application 09556178 and Search Result 20101214_103255_us-09-556-178-3.rpr

GenCore version 6.3
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OM protein - protein search, using sw model

Run on: December 14, 2010, 11:24:11 ; Search time 3 Seconds
(without alignments)
7139.284 Million cell updates/secTitle: US-09-556-178-3
Perfect score: 994
Sequence: 1 NRIWTESEHVFDRFWEIVTTA.....TASAGRTIRTFMAAAFAEK 194Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 segs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summariesDatabase : PIR_80:
1: pir1:
2: pir2:
3: pir3:
4: pir4:

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	390	39.2	209	2 T20975	hypothetical prote
2	275	27.7	184	2 T40305	hypothetical prote
3	270	27.2	230	2 J37798	MGFI protein - yaa
4	231.5	23.3	179	2 J49782	MGFI protein homol
5	213	21.4	215	2 J05048	bromodeoxyuridine-
6	201.5	20.3	175	2 J48546	hypothetical prote
7	185	18.6	171	2 T39247	hypothetical prote
8	184.5	18.6	329	2 J28305	hypothetical prote
9	184.5	18.6	743	2 J88951	protein T2305.2 li
10	117.5	11.8	210	2 T18703	hypothetical prote
11	93	9.4	458	1 J74543	transcription term
12	87	8.8	7962	2 J38346	elastic titin - bu
13	84.5	8.5	667	2 J64017	formate dehydrogen
14	84	8.5	1257	2 J28764	neuracan precursor
15	83.5	8.4	343	2 C95912	hypothetical prote
16	83.5	8.4	1464	2 A43274	N-methyl D-asparta
17	82.5	8.3	694	2 J59040	long-chain-fatty-a
18	82.5	8.3	817	2 J04176	pyruvate, water di
19	82.5	8.3	1015	2 T41111	hypothetical ATP b
20	82.5	8.3	1313	2 J39673	hypothetical prote
21	82	8.2	683	2 J84615	ospi-like retroel
22	82	8.2	958	2 T20621	hypothetical prote
23	81.5	8.2	159	2 J92675	transcription regu
24	81	8.1	248	2 J95067	hypothetical prote
25	81	8.1	578	2 T38775	hypothetical prote
26	81	8.1	985	1 V0L38P	env polyprotein -
27	81	8.1	1464	1 J29159	glutamate receptor
28	80.5	8.1	554	2 T43211	cytoplasmic signal
29	80.5	8.1	585	2 J54812	H-transporting tw
30	80.5	8.1	953	2 A86351	hypothetical prote
31	80	8.0	529	2 T47983	pectinesterase-lik
32	80	8.0	727	2 A22245	hypothetical prote
33	80	8.0	831	2 A11515	ORF4 or listeria s
34	80	8.0	847	2 A48228	beta-N-acetylhexos
35	80	8.0	6713	2 J89921	hypothetical prote
36	79.5	8.0	272	2 T35656	ribonuclease III -
37	79.5	8.0	424	2 T32434	hypothetical prote
38	79.5	8.0	446	1 J082P2	tubulin gamma chai
39	79.5	8.0	512	2 T48462	cytochrome P450-II
40	79.5	8.0	687	2 T09051	PepA protein - Pae
41	79.5	8.0	718	2 T49572	related to SHK1 RI
42	79.5	8.0	319	2 T49729	RD protein - mouse
43	79.5	8.0	5170	2 T15348	hypothetical prote
44	79	7.9	314	2 J97538	ribosomal large ch
45	79	7.9	329	2 AG2757	hypothetical prote

ALIGNMENTS

RESULT 1
T20975
hypothetical protein F1503.6 - Caenorhabditis elegans
C|Species: Caenorhabditis elegans
C|Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #taxt_change 09-Jul-2004
C|Accession: T20975
R|White, S.
submitted to the EMBL Data Library, October 1996
A|Reference number: J19353
A|Accession: T20975
A|Status: preliminary; translated from GB/EMBL/DDBJ
A|Molecule type: DNA
A|Residues: 1-209 «HL»

SCORE Search Results Details for Application 09556178 and Search Result 20101214_103254_us-09-556-178-3.rup.

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OM protein - protein search, using sw model

Run on: December 14, 2010, 11:23:42 ; Search time 106 Seconds
(without alignments)
7637.199 Million cell updates/sec

Title: US-09-556-178-3
Perfect score: 994
Sequence: 1 MKIWTSEHVFDHPWETVTTA.....TASARGTIRTPMAAAFAEK 194

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 12869322 seqs, 4158259533 residues

Total number of hits satisfying chosen parameters: 12869322

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_201011:*
1: uniprot_sprot:*
2: uniprot_trembl:*
SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	994	100.0	194	1	SLMO2_HUMAN	Q9y3b1 RecName: Fu
2	990	99.6	194	1	SLMO2_MACFA	Q4r5s9 RecName: Fu
3	976	98.2	194	1	SLMO2_BOVIN	Q58db0 RecName: Fu
4	955	96.1	194	1	SLMO2_PIG	A5gfx0 RecName: Fu
5	945	95.1	195	1	SLMO2_RAT	Q6p9u4 RecName: Fu
6	943	94.9	195	1	SLMO2_CRIGR	Q6tmk8 RecName: Fu
7	938	94.4	195	1	SLMO2_MOUSE	Q9cyy7 RecName: Fu
8	937	94.3	192	2	D2H1X1_AILME	D2h1x1 SubName: Fu
9	902	90.7	194	2	Q5F3S7_CHICK	Q5f3s7 SubName: Fu
10	870	87.5	194	2	Q63ZN0_XENLA	Q63zn0 SubName: Fu
11	859	86.4	194	2	Q7ZXW8_XENLA	Q7zxw8 SubName: Fu
12	850	85.5	198	2	Q5ZJM8_CHICK	Q5zjm8 SubName: Fu
13	823.5	82.8	193	2	Q7ZVG4_DANRE	Q7zvq4 SubName: Fu
14	820	82.5	164	2	Q5JX17_HUMAN	Q5jx17 SubName: Fu
15	811	81.6	194	2	B5X7V2_SALSA	B5x7v2 SubName: Fu

16	802	80.7	190	2	Q4S9S0_TETNG	Q4s9s0	SubName: Fu
17	798	80.3	189	2	Q4S7Z8_TETNG	Q4s7z8	SubName: Fu
18	796.5	80.1	193	2	B5XGX8_SALSA	B5xgx8	SubName: Fu
19	778	78.3	193	2	C1BX15_ESOLU	C1bx15	SubName: Fu
20	752	75.7	192	2	Q5ZHR9_CHICK	Q5zhr9	SubName: Fu
21	702	70.6	153	2	A0JLN8_MOUSE	A0jln8	SubName: Fu
22	676	68.0	172	2	B0JZX8_XENTR	B0jzx8	SubName: Fu
23	675	67.9	168	2	B5X8X5_SALSA	B5x8x5	SubName: Fu
24	672	67.6	172	1	SLMO1_XENLA	Q6gm21	RecName: Fu
25	653	65.7	172	1	SLMO1_HUMAN	Q96n28	RecName: Fu
26	653	65.7	172	2	D3DUJ1_HUMAN	D3duj1	SubName: Fu
27	647.5	65.1	207	2	C3YFM1_BRAFL	C3yfm1	SubName: Fu
28	635	63.9	172	1	SLMO1_MOUSE	Q8ve85	RecName: Fu
29	634	63.8	172	2	D3ZAN9_RAT	D3zan9	SubName: Fu
30	607	61.1	169	2	C1BK19_OSMMO	C1bk19	SubName: Fu
31	582	58.6	144	2	D2I1R2_AILME	D2i1r2	SubName: Fu
32	558	56.1	151	2	B4E0C9_HUMAN	B4e0c9	SubName: Fu
33	535	53.8	212	2	D1FPK7_CIMLE	D1fpk7	SubName: Fu
34	526.5	53.0	219	2	B4LR10_DROVI	B4lr10	SubName: Fu
35	525.5	52.9	219	2	B4KL67_DROMO	B4kl67	SubName: Fu
36	524	52.7	215	1	SLMO_DROME	Q9v3u9	RecName: Fu
37	524	52.7	215	2	A4V0A1_DROME	A4v0a1	SubName: Fu
38	524	52.7	215	2	B3N9R9_DROER	B3n9r9	SubName: Fu
39	524	52.7	215	2	B4I1Q1_DROSE	B4i1q1	SubName: Fu
40	524	52.7	215	2	B4Q469_DROSI	B4q469	SubName: Fu
41	524	52.7	228	2	Q6PTY2_BOMMO	Q6pty2	SubName: Fu
42	523.5	52.7	219	2	B4MUY1_DROWI	B4muy1	SubName: Fu
43	521	52.4	215	2	B4NZR3_DROYA	B4nzz3	SubName: Fu
44	521	52.4	223	2	D6WM43_TRICA	D6wm43	SubName: Fu
45	517.5	52.1	222	2	B3MKJ3_DROAN	B3mkj3	SubName: Fu

ALIGNMENTS

RESULT 1

SLMO2_HUMAN

ID SLMO2_HUMAN Reviewed; 194 AA.
AC Q9Y3B1; Q9NUL0;
DT 06-DEC-2002, integrated into UniProtKB/Swiss-Prot.
DT 06-DEC-2002, sequence version 2.
DT 02-NOV-2010, entry version 69.
DE RecName: Full=Protein slowmo homolog 2;
GN Name=SLMO2; Synonyms=C20orf45; ORFNames=CGI-107;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RX MEDLINE=20272150; PubMed=10810093; DOI=10.1101/gr.10.5.703;
RA Lai C.-H., Chou C.-Y., Ch'ang L.-Y., Liu C.-S., Lin W.-C.;
RT "Identification of novel human genes evolutionarily conserved in
RT Caenorhabditis elegans by comparative proteomics."
RL Genome Res. 10:703-713(2000).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Placenta;
RX PubMed=14702039; DOI=10.1038/ngl285;
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Oabayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,
RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
RA Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,

RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
RA Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y., Ishida S.,
RA Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,
RA Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O., Nomura Y.,
RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
RA Yushashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohara T., Sano S.,
RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
RT "Complete sequencing and characterization of 21,243 full-length human
RT cDNAs.";
RL Nat. Genet. 36:40-45(2004).
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;
RA Deloukas P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R.,
RA Jones M., Stavridis G., Almeida J.P., Babbage A.K., Bagguley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Copley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Lehtvaeslaiho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Marsh V.L., Martin S.L., McConnell L.J., McLay K., McMurray A.A.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S.,
RA Suke C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Rogers J.;
RT "The DNA sequence and comparative analysis of human chromosome 20.";
RL Nature 414:865-871(2001).
RN [4]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Eye, and Uterus;
RX PubMed=15489334; DOI=10.1101/gr.2596504;
RG The MGC Project Team;
RT "The status, quality, and expansion of the NIH full-length cDNA
RT project: the Mammalian Gene Collection (MGC).";
RL Genome Res. 14:2121-2127(2004).
CC -!- SIMILARITY: Belongs to the slowmo family.
CC -!- SIMILARITY: Contains 1 PRELI/MSF1 domain.
CC -!- SEQUENCE CAUTION:
CC Sequence=AAD34102.1; Type=Frameshift; Positions=192;
CC -----

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 CC -----
 DR EMBL; AF151865; AAD34102.1; ALT_FRAME; mRNA.
 DR EMBL; AK002157; BAA92114.1; -; mRNA.
 DR EMBL; AL109840; CAC09373.1; -; Genomic_DNA.
 DR EMBL; BC010649; AAH10649.1; -; mRNA.
 DR EMBL; BC013969; AAH13969.1; -; mRNA.
 DR IPI; IPI00219778; -.
 DR RefSeq; NP_057129.2; -.
 DR UniGene; Hs.724592; -.
 DR ProteinModelPortal; Q9Y3B1; -.
 DR Ensembl; ENST00000355937; ENSP00000348206; ENSG00000101166.
 DR GeneID; 51012; -.
 DR KEGG; hsa:51012; -.
 DR UCSC; uc002yam.1; human.
 DR CTD; 51012; -.
 DR GeneCards; GC20M057608; -.
 DR H-InvDB; HIX0203035; -.
 DR HGNC; HGNC:15892; SLMO2.
 DR HPA; CAB017039; -.
 DR HOGENOM; HBG602019; -.
 DR HOVERGEN; HBG009393; -.
 DR InParanoid; Q9Y3B1; -.
 DR OMA; AAWRKYP; -.
 DR OrthoDB; EOG92FW2T; -.
 DR PhylomeDB; Q9Y3B1; -.
 DR NextBio; 53504; -.
 DR ArrayExpress; Q9Y3B1; -.
 DR Bgee; Q9Y3B1; -.
 DR CleanEx; HS_SLMO2; -.
 DR Genevestigator; Q9Y3B1; -.
 DR GermOnline; ENSG00000101166; Homo sapiens.
 DR InterPro; IPR006797; PRELI/MSF1.
 DR Pfam; PF04707; PRELI; 1.
 DR PROSITE; PS50904; PRELI_MSFL; 1.
 PE 1: Evidence at protein level;
 KW Complete proteome.
 FT CHAIN 1 194 Protein slowmo homolog 2.
 FT /FTId=PRO_0000079429.
 FT DOMAIN 1 172 PRELI/MSFL.
 SQ SEQUENCE 194 AA; 21495 MW; DF32EA44992BFA94 CRC64;

Query Match 100.0%; Score 994; DB 1; Length 194;
 Best Local Similarity 100.0%;
 Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKIINTSEHVDPHPWETVTTAAMQKYPNPMNPSVVGVDVDRHIDPSGKLHSHRLLSTEWG 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1 MKIINTSEHVDPHPWETVTTAAMQKYPNPMNPSVVGVDVDRHIDPSGKLHSHRLLSTEWG 60

 Qy 61 LPSIVKSLIGAARTKTYVQEHSSVVDPEKTMELKSTNISFTNMVSDERLIYKPHPQDPE 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 61 LPSIVKSLIGAARTKTYVQEHSSVVDPEKTMELKSTNISFTNMVSDERLIYKPHPQDPE 120

 Qy 121 KTVLTQEAIIITVKGVSLSYLEGLMASTISSNASKGREAMEWVHKLNABEELTASARG 180
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 121 KTVLTQEAIIITVKGVSLSYLEGLMASTISSNASKGREAMEWVHKLNABEELTASARG 180

 Qy 181 TIRTPMAAAFAEK 194
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 Db 181 TIRTPMAAAFAEK 194

RESULT 2
 SLMO2_MACFA
 ID SLMO2_MACFA Reviewed; 194 AA.

DT 08-APR-2008, integrated into UniProtKB/Swiss-Prot.
 DT 05-JUL-2004, sequence version 1.
 DT 20-APR-2010, entry version 30.
 DE RecName: Full=Protein slowmo homolog 2;
 GN Name=Slmo2;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muroidea; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC TISSUE=Pituitary;
 RX PubMed=15489334; DOI=10.1101/gr.2596504;
 RG The MGC Project Team;
 RT "The status, quality, and expansion of the NIH full-length cDNA
 RT project: the Mammalian Gene Collection (MGC).";
 RL Genome Res. 14:2121-2127(2004).
 CC -!- SIMILARITY: Belongs to the slowmo family.
 CC -!- SIMILARITY: Contains 1 PRELI/MSF1 domain.
 CC -----
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 CC -----
 DR EMBL; BC060590; AAH60590.1; -; mRNA.
 DR IPI; IPI00454393; -.
 DR RefSeq; NP_001009543.1; -.
 DR UniGene; Rn.185814; -.
 DR GeneID; 494346; -.
 DR KEGG; rno:494346; -.
 DR RGD; 1594395; MGC72955.
 DR eggNOG; roNOG16291; -.
 DR HOVERGEN; HBG009393; -.
 DR PhylomeDB; Q6P9U4; -.
 DR NextBio; 697627; -.
 DR Genevestigator; Q6P9U4; -.
 DR InterPro; IPR006797; PRELI/MSF1.
 DR Pfam; PF04707; PRELI; 1.
 DR PROSITE; PS50904; PRELI_MSFL; 1.
 PE 2: Evidence at transcript level;
 FT CHAIN 1 195 Protein slowmo homolog 2.
 FT /FTid=PRO_0000327685.
 FT DOMAIN 1 172 PRELI/MSFL.
 SQ SEQUENCE 195 AA; 21572 MW; E56281ED13960AD4 CRC64;

Query Match 95.1%; Score 945; DB 1; Length 195;
 Best Local Similarity 95.3%;
 Matches 181; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

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Qy      1 MKIWTSEHVFDHPWETVTTAAMQKYPNPMNPSVVGVDVLDLRHIDPSGKLHSHRLLSTEWG 60
      |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      1 MKIWTSEHVFDHPWETVTTAAMQKYPNPMNPSVVGVDVLDLRHVDPSGKLHSHRLLSTEWG 60

Qy     61 LPSIVKSLIGAARTKTYVQEHSVVDPVEKTMELKSTNISFTNMVSVDERLIYKPHQDPE 120
      |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db     61 LPSIVKSLIGAARTKTYVQEHSVVDPPIRRTMELKSTNISFTNMVSVDERLIYKPHQDPE 120

Qy     121 KTVLTQEALITVKGVSLSYLEGLMASTISSNASKGREAMEWVIHKLNAEIEELTASARG 180
      |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db     121 KTVLTQEALITVKGVSLSYLEGLMASTISSNANKGREAMEWVIHKLNAEIEELTASARG 180

Qy     181 TIRTPMAAAA 190
      :|||||||
Db     181 SIRTPMAAAA 190
  
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RESULT 6

SLMO2_CRIGR
ID SLMO2_CRIGR Reviewed; 195 AA.
AC Q6TMK8;
DT 08-APR-2008, integrated into UniProtKB/Swiss-Prot.
DT 05-JUL-2004, sequence version 1.
DT 02-MAR-2010, entry version 15.
DE RecName: Full=Protein slowmo homolog 2;
DE AltName: Full=BCR/ABL-regulated protein;
GN Name=SLMO2;
OS Cricetulus griseus (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Cricetidae; Cricetinae; Cricetulus.
OX NCBI_TaxID=10029;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RC TISSUE=Ovary;
RA Guang L., Masabumi S., Maru Y.;
RT "Differential display analysis of BCR/ABL-regulated genes."
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the slowmo family.
CC -!- SIMILARITY: Contains 1 PRELI/MSF1 domain.
CC -----
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AY392425; AAQ94084.1; -, mRNA.
DR HOVERGEN; HBG009393; -.
DR InterPro; IPR006797; PRELI/MSF1.
DR Pfam; PF04707; PRELI; 1.
DR PROSITE; PS50904; PRELI_MSFL; 1.
PE 2: Evidence at transcript level;
FT CHAIN 1 195 Protein slowmo homolog 2.
FT /FTId=PRO_0000327686.
FT DOMAIN 1 172 PRELI/MSF1.
SQ SEQUENCE 195 AA; 21532 MW; C59335DE152049C7 CRC64;

Query Match 94.9%; Score 943; DB 1; Length 195;
Best Local Similarity 95.8%;
Matches 182; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MKIWTSEHVFDPHPWETVTTAAMQKYPNPMNPSVVGVDVLDRLHIDPSGKLHSHRLLSTEWG 60
Db 1 MKIWTSEHVFDPHPWEMVTTAAMQKYPNPMNPSVVGVDVLDRLHIDPSGKLHSHRLLSTEWG 60
Qy 61 LPSIVKSLIGAARTKTYVQEHVSVDVPVKTMELKSTNISFTNMVSDERLIYKPHQPDPE 120
Db 61 LPSIVKSLIGAARTKTYVQEHVSVDVPVKTMELKSTNISFTNMVSDERLIYKPHQPDPE 120
Qy 121 KTVLTQEAIIYTKVGSLSYLEGLMASTISSNASKGREAMEWVIHKLNAEIELTASARG 180
Db 121 KTVLTQEAIIYTKVGSLSYLEGLMASTISSNANKGREAMEWVIHKLNAEIEDLAASARG 180
Qy 181 TIRTPMAAAA 190
Db 181 SIRTPMAAAA 190

RESULT 7

SLMO2_MOUSE
ID SLMO2_MOUSE Reviewed; 195 AA.
AC Q9CY7; A2ADM7; Q3UC64; Q9CRD3;
DT 06-DEC-2002, integrated into UniProtKB/Swiss-Prot.
DT 06-DEC-2002, sequence version 2.
DT 05-OCT-2010, entry version 61.
DE RecName: Full=Protein slowmo homolog 2;
GN Name=Slmo2;

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muroidea; Muridae; Murinae; Mus; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC STRAIN=C57BL/6J;
 RC TISSUE=Bone marrow macrophage, Brain, and Small intestine;
 RX PubMed=16141072; DOI=10.1126/science.1112014;
 RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
 RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
 RA Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
 RA Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
 RA Ambesi-Impombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
 RA Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
 RA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
 RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
 RA di Bernardo D., Down T., Engstrom P., Fagioli M., Faulkner G.,
 RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
 RA Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
 RA Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
 RA Hill D., Huminicki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
 RA Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
 RA Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
 RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
 RA Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
 RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
 RA Mottagui-Tabar S., Mulder N., Nakano N., Nakauchi H., Ng P.,
 RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
 RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavesi G., Pesole G.,
 RA Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
 RA Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
 RA Schoenbach C., Sekiguchi K., Sempere C.A., Seno S., Sessa L., Sheng Y.,
 RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
 RA Sperling S., Stupka E., Sugiura K., Sultana R., Takenaka Y., Taki K.,
 RA Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
 RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
 RA Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
 RA Grimmond S.M., Teasdale R.D., Liu E.T., Bruscia V., Quackenbush J.,
 RA Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
 RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
 RA Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
 RA Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
 RA Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
 RA Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
 RA Hayashizaki Y.;
 RT "The transcriptional landscape of the mammalian genome."
 RL Science 309:1559-1563(2005).
 RN [2]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=C57BL/6J;
 RX PubMed=19468303; DOI=10.1371/journal.pbio.1000112;
 RA Church D.M., Goodstadt L., Hillier L.W., Zody M.C., Goldstein S.,
 RA She X., Bult C.J., Agarwala R., Cherry J.L., DiCuccio M., Hlavina W.,
 RA Kapustin Y., Meric P., Maglott D., Birtle Z., Marques A.C., Graves T.,
 RA Zhou S., Teague B., Potamousis K., Churas C., Place M., Herschleb J.,
 RA Runnheim R., Forrest D., Amos-Landgraf J., Schwartz D.C., Cheng Z.,
 RA Lindblad-Toh K., Eichler E.E., Ponting C.P.;
 RT "Lineage-specific biology revealed by a finished genome assembly of
 the mouse."
 RL PLoS Biol. 7:E1000112-E1000112(2009).
 RN [3]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC TISSUE=Kidney;
 RX PubMed=15489334; DOI=10.1101/gr.2596504;
 RG The MGC Project Team;

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RT      "The status, quality, and expansion of the NIH full-length cDNA
RT      project: the Mammalian Gene Collection (MGC).";
RL      Genome Res. 14:2121-2127(2004).
CC      -!- SIMILARITY: Belongs to the slowmo family.
CC      -!- SIMILARITY: Contains 1 PRELI/MSF1 domain.
CC      -----
CC      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
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CC      -----
DR      EMBL; AK003043; BAB22528.1; -; mRNA.
DR      EMBL; AK008542; BAB25731.1; -; mRNA.
DR      EMBL; AK150668; BAE29750.1; -; mRNA.
DR      EMBL; AL670951; CAM26665.1; -; Genomic_DNA.
DR      EMBL; BC026968; AAH26968.1; -; mRNA.
DR      IPI; IPI00112243; -.
DR      RefSeq; NP_079807.1; -.
DR      UniGene; Mm.479169; -.
DR      ProteinModelPortal; Q9CY7; -.
DR      PRIDE; Q9CY7; -.
DR      Ensembl; ENSMUST00000016401; ENSMUSP00000016401; ENSMUSG00000016257.
DR      GeneID; 66390; -.
DR      KEGG; mmu:66390; -.
DR      UCSC; uc008ofg.1; mouse.
DR      CTD; 66390; -.
DR      MGI; MGI:1913640; Slmo2.
DR      HOGENOM; HBG602019; -.
DR      HOVERGEN; HBG009393; -.
DR      InParanoid; Q9CY7; -.
DR      OMA; AAWRKYP; -.
DR      OrthoDB; EOG92FW2T; -.
DR      PhylomeDB; Q9CY7; -.
DR      NextBio; 321529; -.
DR      ArrayExpress; Q9CY7; -.
DR      Bgee; Q9CY7; -.
DR      CleanEx; MM_SLM02; -.
DR      Genevestigator; Q9CY7; -.
DR      GermOnline; ENSMUSG00000016257; Mus musculus.
DR      GO; GO:0005739; C:mitochondrion; IDA:MGI.
DR      InterPro; IPR006797; PRELI/MSF1.
DR      Pfam; PF04707; PRELI; 1.
DR      PROSITE; PS50904; PRELI_MSFI; 1.
PE      2: Evidence at transcript level;
FT      CHAIN             1           195           Protein slowmo homolog 2.
FT                                     /FTid=PRO_0000079430.
FT      DOMAIN             1           172           PRELI/MSF1.
FT      CONFLICT           194          194          D -> N (in Ref. 1; BAE29750).
SQ      SEQUENCE          195 AA;   21492 MW;   003CDA86C29E6779 CRC64;

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Query Match 94.4%; Score 938; DB 1; Length 195;
 Best Local Similarity 95.8%;
 Matches 182; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

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Qy      1 MKIINTSEHVFDPHWETVTTAAMQKYPNPMNPSVVGVDVLDLRHIDPSGKLHSHRLLSTEWG 60
Db      1 MKIINTSEHVFDPHWETVTTAAMQKYPNPMNPSVVGVDVLDLRHVDPSGKLHSHRLLSTEWG 60

Qy      61 LPSIVKSLIGAARTKTYVQEHSSVDPVEKTMELKSTNISFTNMVSVDERLIYKPHQDPE 120
Db      61 LPSIVKSLIGAARTKTYVQEHSSVDPVTRTMELKSTNISFTNMVSVDERLIYKPHLQDPE 120

Qy      121 KTVLTQEAIITVKGVSLSSYLEGLMASTISSNASKGREAMEWVIHKLNAEIEELTASARG 180
Db      121 KTVLTQEAIITVKGVSLSSYLEGLMASTISSNASKGREAMEWVIHKLNAEIEELAASARG 180

Qy      181 TIRTPMAAAA 190
Db      181 SIRTPMAAAA 190

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RESULT 8

D2H1X1_AILME

ID D2H1X1_AILME Unreviewed; 192 AA.

AC D2H1X1;

DT 09-FEB-2010, integrated into UniProtKB/TrEMBL.

DT 09-FEB-2010, sequence version 1.

DT 20-APR-2010, entry version 3.

DE SubName: Full=Putative uncharacterized protein;

DE Flags: Fragment;

GN ORFNames=PANDA_003568;

OS Ailuropoda melanoleuca (Giant panda).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Caniformia; Ursidae;

OC Ailuropoda.

OX NCBI_TaxID=9646;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RX PubMed=20010809; DOI=10.1038/nature08696;

RA Li R., Fan W., Tian G., Zhu H., He L., Cai J., Huang Q., Cai Q.,

RA Li B., Bai Y., Zhang Z., Zhang Y., Wang W., Li J., Wei F., Li H.,

RA Jian M., Li J., Zhang Z., Nielsen R., Li D., Gu W., Yang Z., Xuan Z.,

RA Ryder O.A., Leung F.C., Zhou Y., Cao J., Sun X., Fu Y., Fang X.,

RA Guo X., Wang B., Hou R., Shen F., Mu B., Ni P., Lin R., Qian W.,

RA Wang G., Yu C., Nie W., Wang J., Wu Z., Liang H., Min J., Wu Q.,

RA Cheng S., Ruan J., Wang M., Shi Z., Wen M., Liu B., Ren X., Zheng H.,

RA Dong D., Cook K., Shan G., Zhang H., Kosiol C., Xie X., Lu Z.,

RA Zheng H., Li Y., Steiner C.C., Lam T.T., Lin S., Zhang Q., Li G.,

RA Tian J., Gong T., Liu H., Zhang D., Fang L., Ye C., Zhang J., Hu W.,

RA Xu A., Ren Y., Zhang G., Bruford M.W., Li Q., Ma L., Guo Y., An N.,

RA Hu Y., Zheng Y., Shi Y., Li Z., Liu Q., Chen Y., Zhao J., Qu N.,

RA Zhao S., Tian F., Wang X., Wang H., Xu L., Liu X., Vinar T., Wang Y.,

RA Lam T.W., Yiu S.M., Liu S., Zhang H., Li D., Huang Y., Wang X.,

RA Yang G., Jiang Z., Wang J., Qin N., Li L., Li J., Bolund L.,

RA Kristiansen K., Wong G.K., Olson M., Zhang X., Li S., Yang H.,

RA Wang J., Wang J.;

RT "The sequence and de novo assembly of the giant panda genome.";

RL Nature 463:311-317(2010).

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 CC -----

DR EMBL; GL192436; EFB24009.1; -; Genomic_DNA.

DR InterPro; IPR006797; PRELI/MSF1.

DR Pfam; PF04707; PRELI; 1.

DR PROSITE; PS50904; PRELI_MSFI; 1.

PE 4: Predicted;

FT NON_TER 1 1

FT NON_TER 192 192

SQ SEQUENCE 192 AA; 21186 MW; 122A162343776DC7 CRC64;

Query Match 94.3%; Score 937; DB 2; Length 192;

Best Local Similarity 95.3%;

Matches 183; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

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Qy      3  IWTSEHVFDHPWETVTTAAMQKYPNPMNPSVVGVDVLDRIHIDPSGKLHSHRLLSTEWGLP 62
       :|  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
Db      1  VWFVLVGHGHPWETVTTAAMQKYPNPMNPSVVGVDVLDRIHIDPSGKLHSHRLLSTEWGLP 60

Qy     63  SIVKSLIGAARTKTYVQEHSSVVDPEKTMELKSTNISFTNMVSVDERLIYKHPHPDQPEKT 122
       ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
Db     61  SIVKSLIGAARTKTYVQEHSSVVDPEKTMELKSTNISFTNMVSVDERLIYKHPHPDQPEKT 120

Qy     123  VLTQEAIIIVKGVSLSSYLEGLMASTISSNASKGREAMEVWIHKLNAEIEELTASARGTI 182
       ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
Db     121  VLTQEAIIIVKGVSLSSYLEGLMASTISSNANKGREAMEVWIHKLNAEIEELTASARGSI 180

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Qy 183 RTPMAAAFAEK 194
 Db 181 RTPMAAAFVEK 192

RESULT 9

Q5F3S7_CHICK

ID Q5F3S7_CHICK Unreviewed; 194 AA.
 AC Q5F3S7;
 DT 15-MAR-2005, integrated into UniProtKB/TrEMBL.
 DT 15-MAR-2005, sequence version 1.
 DT 05-OCT-2010, entry version 21.
 DE SubName: Full=Putative uncharacterized protein;
 GN ORFNames=RCJMB04_7n6;
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Dinosauria; Saurischia; Theropoda; Coelurosauria; Aves;
 OC Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=CB; TISSUE=Bursa;
 RA Caldwell R.B., Kierzek A.M., Arakawa H., Bezzubov Y., Zaim J.,
 RA Fiedler P., Kutter S., Blagodatski A., Kostovska D., Koter M.,
 RA Plachy J., Carninci P., Hayashizaki Y., Buerstedde J.M.;
 RT "Full-length cDNAs from chicken bursal lymphocytes to facilitate
 RT genefunction analysis."
 RL Genome Biol. 6:R6-R6(2005).
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 CC -----
 DR EMBL; AJ851573; CAH65207.1; -; mRNA.
 DR IPI; IPI00680122; -.
 DR RefSeq; NP_001026037.1; -.
 DR UniGene; Gga.9900; -.
 DR Ensembl; ENSGALT000000022444; ENSGALP000000022404; ENSGALG00000007439.
 DR GeneID; 419310; -.
 DR KEGG; gga:419310; -.
 DR CTD; 419310; -.
 DR eggNOG; veNOG05438; -.
 DR HOVERGEN; HBG009393; -.
 DR PhylomeDB; Q5F3S7; -.
 DR InterPro; IPR006797; PRELI/MSF1.
 DR Pfam; PF04707; PRELI; 1.
 DR PROSITE; PS0904; PRELI_MSFI; 1.
 PE 2: Evidence at transcript level;
 SQ SEQUENCE 194 AA; 21631 MW; 2374E078F78944AF CRC64;

Query Match 90.7%; Score 902; DB 2; Length 194;
 Best Local Similarity 87.6%;
 Matches 170; Conservative 17; Mismatches 7; Indels 0; Gaps 0;

Qy 1 MKIINTSEHVFDHPWETVTTAAMQKYPNPMNPSVVGVDVLDLRHIDSPGKLHSHRLLSTEWG 60
 Db 1 MKIINTSEHVFDHPWETVTTAAMQKYPNPMNPSVVGVDVLDLRHIDSSGKLHSHRLLSTEWG 60

Qy 61 LPSIVKSLIGAARTKTYVQEHSSVVDPEKTMELKSTNISFTNMVSDVERLIYKPHQDPE 120
 Db 61 IPSIVKSLIGTSRTKTYVQEHSSVVDPEKTMELKSSNISFTNLVSDVERLIYKPHQDPE 120

Qy 121 KTVLTQEAIIITVKGVSLSYSLEGLMASTISSNASKGREAMEWVWIKHNAEIEELTASARG 180
 Db 121 KTVLTQEAIIISVKGVSLSYSLEGLMANTISSNANKGREALEWVWIRLNAEIEELTASARG 180

Qy 181 TIRTPMAAAFAEK 194

Q63ZNO_XENLA

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Q63ZNO_XENLA      Unreviewed;              194 AA.
AC   Q63ZNO;
DT   25-OCT-2004, integrated into UniProtKB/TrEMBL.
DT   25-OCT-2004, sequence version 1.
DT   05-OCT-2010, entry version 25.
DE   SubName: Full=LOC494772 protein;
GN   Name=slmo2; Synonyms=LOC494772;
OS   Xenopus laevis (African clawed Frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC   Xenopodinae; Xenopus; Xenopus.
OX   NCBI_TaxID=83355;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   TISSUE=Eye;
RG   NIH - Xenopus Gene Collection (XGC) project;
RL   Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
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DR   EMBL; BC082882; AAH82882.1; -. mRNA.
DR   RefSeq; NP_001088075.1; -.
DR   UniGene; XL14591; -.
DR   GeneID; 494772; -.
DR   KEGG; xla:494772; -.
DR   CTD; 494772; -.
DR   Xenbase; XB-GENE-5919530; slmo2.
DR   HOVERGEN; HBG009393; -.
DR   InterPro; IPR006797; PRELI/MSF1.
DR   Pfam; PF04707; PRELI; 1.
DR   PROSITE; PS50904; PRELI_MSF1; 1.
PE   2: Evidence at transcript level;
SQ   SEQUENCE   194 AA;  21533 MW;  8E8BA6F811EB8846 CRC64;

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Best Local Similarity 85.6%;
Matches 166; Conservative 18; Mismatches 10; Indels 0; Gaps 0;

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Db	1	MRIWTSEHVFDHPNETVTTAAMQKYPNPMNPVSVGVGDVLDNRHIDPSGKGLHSDRLSTEWG	60
Qy	61	LPSIVKSLIGAARTKTYVQEHSSVDPVEKTMELKSTNISFTNMVSDVERLIYKHPHQDPE	120
Db	61	MPSLVKSIIGASRTKTYVQEHSSVDPVERTMELESSNITFTNMVSDVERLIYKHPHQDPG	120
Qy	121	KTVLTQEAIITVKGVSLSYLEGLMASTISSNASKGREAMEWVIHKLNAEIEELTASARG	180
Db	121	KTVLTQEAIIVAKGVSLSSYLEGMMANTISSNANKGRDAMEWVIGRLNAEIEDLKASTRS	180
Qy	181	TIRTPMAAAFAEK	194
Db	181	SIRSSMAAAFLK	194

Q7ZXW8_XENLA

ID Q7ZXW8_XENLA Unreviewed; 194 AA.
AC Q7ZXW8;
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.

SCORE Search Results Details for Application 09556178 and Search Result 20101214_103255_us-09-556-178-3.ra1.

[Score Home Page](#) [Retrieve Application List](#) [SCORE System Overview](#) [SCORE FAQ](#) [Comments / Suggestions](#)

This page gives you Search Results detail for the Application 09556178 and Search Result 20101214_103255_us-09-556-178-3.ra1.

[Go Back to previous page](#)

GenCore version 6.3
Copyright (c) 1993 - 2010 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: December 14, 2010, 11:24:20 ; Search time 27 Seconds
(without alignments)
2826.599 Million cell updates/sec

Title: US-09-556-178-3
Perfect score: 994
Sequence: 1 MKIWTSEHVDFHPWETVTTA.....TASARGTIRTPMAAAFAEK 194

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2170800 seqs, 396181022 residues

Total number of hits satisfying chosen parameters: 2170800

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /ABSS/Data/CRF/ptodata/1/iaa/5_COMB.pep:*
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4: /ABSS/Data/CRF/ptodata/1/iaa/H_COMB.pep:*
5: /ABSS/Data/CRF/ptodata/1/iaa/PCTUS_COMB.pep:*
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SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	994	100.0	194	1	US-08-967-364-3	Sequence 3, Appli
2	994	100.0	194	2	US-09-368-408-3	Sequence 3, Appli
3	994	100.0	194	3	US-11-443-428A-833084	Sequence 833084,
4	994	100.0	194	3	US-11-443-428A-833085	Sequence 833085,
5	994	100.0	194	3	US-11-443-428A-833086	Sequence 833086,
6	994	100.0	194	3	US-11-443-428A-833087	Sequence 833087,
7	994	100.0	194	3	US-11-443-428A-833088	Sequence 833088,
8	994	100.0	194	3	US-11-443-428A-833089	Sequence 833089,
9	994	100.0	194	3	US-11-443-428A-833091	Sequence 833091,
10	994	100.0	194	3	US-11-443-428A-833093	Sequence 833093,

11	994	100.0	194	3	US-11-443-428A-833095	Sequence 833095,
12	994	100.0	194	3	US-11-443-428A-833099	Sequence 833099,
13	935	94.1	184	3	US-11-443-428A-833098	Sequence 833098,
14	903.5	90.9	179	3	US-11-443-428A-833097	Sequence 833097,
15	891	89.6	176	3	US-11-443-428A-833092	Sequence 833092,
16	820	82.5	164	3	US-11-443-428A-833090	Sequence 833090,
17	653	65.7	172	2	US-10-094-749-2348	Sequence 2348, Ap
18	601	60.5	207	3	US-11-443-428A-779447	Sequence 779447,
19	511	51.4	104	3	US-11-443-428A-833096	Sequence 833096,
20	369	37.1	136	3	US-11-443-428A-779446	Sequence 779446,
21	369	37.1	136	3	US-11-443-428A-779448	Sequence 779448,
22	321	32.3	59	2	US-09-513-999C-6276	Sequence 6276, Ap
23	321	32.3	59	3	US-10-793-479-6276	Sequence 6276, Ap
24	241.5	24.3	196	3	US-11-241-607-63745	Sequence 63745, A
25	234.5	23.6	196	3	US-10-767-701-35425	Sequence 35425, A
26	233.5	23.5	196	3	US-11-241-607-55193	Sequence 55193, A
27	233.5	23.5	196	3	US-11-241-607-57633	Sequence 57633, A
28	213	21.4	215	1	US-08-796-676-3	Sequence 3, Appli
29	213	21.4	215	1	US-08-967-364-8	Sequence 8, Appli
30	213	21.4	215	2	US-09-368-408-8	Sequence 8, Appli
31	213	21.4	215	2	US-09-213-391-3	Sequence 3, Appli
32	201.5	20.3	208	3	US-11-443-428A-897564	Sequence 897564,
33	200.5	20.2	208	3	US-11-443-428A-897563	Sequence 897563,
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35	200.5	20.2	219	2	US-09-213-391-1	Sequence 1, Appli
36	200.5	20.2	219	3	US-11-443-428A-897559	Sequence 897559,
37	200.5	20.2	219	3	US-11-443-428A-897560	Sequence 897560,
38	200.5	20.2	219	3	US-11-443-428A-897562	Sequence 897562,
39	200.5	20.2	219	3	US-11-443-428A-897569	Sequence 897569,
40	200.5	20.2	219	3	US-11-443-428A-897571	Sequence 897571,
41	200.5	20.2	219	3	US-11-443-428A-1031541	Sequence 1031541,
42	200.5	20.2	249	3	US-11-443-428A-897570	Sequence 897570,
43	200.5	20.2	249	3	US-11-443-428A-897572	Sequence 897572,
44	197.5	19.9	296	3	US-11-443-428A-1031544	Sequence 1031544,
45	195.5	19.7	299	3	US-11-443-428A-897573	Sequence 897573,

ALIGNMENTS

RESULT 1

US-08-967-364-3

; Sequence 3, Application US/08967364

; Patent No. 5989859

; GENERAL INFORMATION:

; APPLICANT: Bandman, Olga

; APPLICANT: Lal, Preeti

; APPLICANT: Guegler, Karl J.

; APPLICANT: Shah, Purvi

; APPLICANT: Corley, Neil C.

; TITLE OF INVENTION: VESICLE TRAFFICKING PROTEINS

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Incyte Pharmaceuticals, Inc.

; STREET: 3174 Porter Dr.

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/967,364

; FILING DATE: No. 5989859ember 7, 1997

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Cerrone, Michael C.
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PF-0417 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 194 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: 2056691
; CLONE: BEPINOT01
US-08-967-364-3

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Query Match          100.0%; Score 994; DB 1; Length 194;
Best Local Similarity 100.0%;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      61 LPSIVKSLIGAARTKTYVQEHSVVDPVEKTMELKSTNISFTNMVSVDERLIYKPHQDPE 120
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Db      61 LPSIVKSLIGAARTKTYVQEHSVVDPVEKTMELKSTNISFTNMVSVDERLIYKPHQDPE 120

Qy      121 KTVLTQEAIITVKGVSLSYLEGLMASTISSNASKGREAMEWVIHKLNAEIEELTASARG 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 KTVLTQEAIITVKGVSLSYLEGLMASTISSNASKGREAMEWVIHKLNAEIEELTASARG 180

Qy      181 TIRTPMAAAFAEK 194
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Db      181 TIRTPMAAAFAEK 194

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RESULT 2
US-09-368-408-3
; Sequence 3, Application US/09368408
; Patent No. 6071703
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Lal, Preeti
; APPLICANT: Guegler, Karl J.
; APPLICANT: Shah, Purvi
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: VESICLE TRAFFICKING PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/09/368,408
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/967,364
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Cerrone, Michael C.
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PF-0417 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 194 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: 2056691
; CLONE: BEP1NOT01
US-09-368-408-3

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Query Match          100.0%; Score 994; DB 2; Length 194;
Best Local Similarity 100.0%;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3

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US-11-443-428A-833084
; Sequence 833084, Application US/11443428A
; Patent No. 7745391
; GENERAL INFORMATION:
; APPLICANT: Mintz, Liat
; APPLICANT: Xie, Hanqing
; APPLICANT: Dahari, Dvir
; APPLICANT: Levanon, Erez
; APPLICANT: Freilich, Shiri
; APPLICANT: Beck, Nili
; APPLICANT: Zhu, Wei-Yong
; APPLICANT: Wasserman, Alon
; APPLICANT: Hermesh, Chen
; APPLICANT: Azar, Idit
; APPLICANT: Bernstein, Jeanne
; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
; FILE REFERENCE: 02/23929
; CURRENT APPLICATION NUMBER: US/11/443,428A
; CURRENT FILING DATE: 2006-05-31
; NUMBER OF SEQ ID NOS: 1034312
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 833084

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Db      121 KTVLTQEAIIIVKGVSLSSYLEGLMASTISSNASKGREAMEWVVIHKLNAEIEELTASARG 180
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Qy      181 TIRTPMAAAFAEK 194
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Db      181 TIRTPMAAAFAEK 194

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RESULT 5
US-11-443-428A-833086
; Sequence 833086, Application US/11443428A
; Patent No. 7745391
; GENERAL INFORMATION:
; APPLICANT: Mintz, Liat
; APPLICANT: Xie, Hanqing
; APPLICANT: Dahari, Dvir
; APPLICANT: Levanon, Erez
; APPLICANT: Freilich, Shiri
; APPLICANT: Beck, Nili
; APPLICANT: Zhu, Wei-Yong
; APPLICANT: Wasserman, Alon
; APPLICANT: Hermesh, Chen
; APPLICANT: Azar, Idit
; APPLICANT: Bernstein, Jeanne
; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
; FILE REFERENCE: 02/23929
; CURRENT APPLICATION NUMBER: US/11/443,428A
; CURRENT FILING DATE: 2006-05-31
; NUMBER OF SEQ ID NOS: 1034312
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 833086
; LENGTH: 194
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-443-428A-833086

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Best Local Similarity 100.0%;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      61 LPSIVKSLIGAARTKTYVQEHSVVDPVEKTMELKSTNISFTNMVSVDERLIYKPHPQDPE 120
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; Sequence 833087, Application US/11443428A
; Patent No. 7745391
; GENERAL INFORMATION:
; APPLICANT: Mintz, Liat
; APPLICANT: Xie, Hanqing
; APPLICANT: Dahari, Dvir
; APPLICANT: Levanon, Erez
; APPLICANT: Freilich, Shiri

```



```

; APPLICANT: Beck, Nili
; APPLICANT: Zhu, Wei-Yong
; APPLICANT: Wasserman, Alon
; APPLICANT: Hermesh, Chen
; APPLICANT: Azar, Idit
; APPLICANT: Bernstein, Jeanne
; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
; FILE REFERENCE: 02/23929
; CURRENT APPLICATION NUMBER: US/11/443,428A
; CURRENT FILING DATE: 2006-05-31
; NUMBER OF SEQ ID NOS: 1034312
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 833087
; LENGTH: 194
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-443-428A-833087

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Query Match          100.0%; Score 994; DB 3; Length 194;
Best Local Similarity 100.0%;
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Qy     61 LPSIVKSLIGAARTKTYVQEHSVVDPVEKTMELKSTNISFTNMVSVDERLIYKPHQDPDE 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 LPSIVKSLIGAARTKTYVQEHSVVDPVEKTMELKSTNISFTNMVSVDERLIYKPHQDPDE 120

Qy    121 KTVLTQEAIITVKGVSLSSYLEGLMASTISSNASKGREAMEWVIHKLNAEIEELTASARG 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 KTVLTQEAIITVKGVSLSSYLEGLMASTISSNASKGREAMEWVIHKLNAEIEELTASARG 180

Qy    181 TIRTPMAAAFAEK 194
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Db    181 TIRTPMAAAFAEK 194

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RESULT 7

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US-11-443-428A-833088
; Sequence 833088, Application US/11443428A
; Patent No. 7745391
; GENERAL INFORMATION:
; APPLICANT: Mintz, Liat
; APPLICANT: Xie, Hangqing
; APPLICANT: Dahari, Dvir
; APPLICANT: Levanon, Erez
; APPLICANT: Freilich, Shiri
; APPLICANT: Beck, Nili
; APPLICANT: Zhu, Wei-Yong
; APPLICANT: Wasserman, Alon
; APPLICANT: Hermesh, Chen
; APPLICANT: Azar, Idit
; APPLICANT: Bernstein, Jeanne
; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
; FILE REFERENCE: 02/23929
; CURRENT APPLICATION NUMBER: US/11/443,428A
; CURRENT FILING DATE: 2006-05-31
; NUMBER OF SEQ ID NOS: 1034312
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 833088
; LENGTH: 194
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-443-428A-833088

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Query Match          100.0%; Score 994; DB 3; Length 194;
Best Local Similarity 100.0%;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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      |||
Db      1 MKIWTSEHVFDPHPWETVTTAAMQKYPNPMNPSVVGVDVDRHIDPSGKLHSHRLLSTEWG 60

Qy      61 LPSIVKSLIGAARTKTYVQEHSSVVDPEKTMELKSTNISFTNMVSVDERLIYKPHQDPE 120
      |||
Db      61 LPSIVKSLIGAARTKTYVQEHSSVVDPEKTMELKSTNISFTNMVSVDERLIYKPHQDPE 120

Qy      121 KTVLTQEAIITVKGVSLSYLEGLMASTISSNASKGREAMEWVIHKLNAEIEELTASARG 180
      |||
Db      121 KTVLTQEAIITVKGVSLSYLEGLMASTISSNASKGREAMEWVIHKLNAEIEELTASARG 180

Qy      181 TIRTPMAAAFAEK 194
      |||
Db      181 TIRTPMAAAFAEK 194

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RESULT 8

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US-11-443-428A-833089
; Sequence 833089, Application US/11443428A
; Patent No. 7745391
; GENERAL INFORMATION:
; APPLICANT: Mintz, Liat
; APPLICANT: Xie, Hanqing
; APPLICANT: Dahari, Dvir
; APPLICANT: Levanon, Erez
; APPLICANT: Freilich, Shiri
; APPLICANT: Beck, Nili
; APPLICANT: Zhu, Wei-Yong
; APPLICANT: Wasserman, Alon
; APPLICANT: Hermesh, Chen
; APPLICANT: Azar, Idit
; APPLICANT: Bernstein, Jeanne
; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
; FILE REFERENCE: 02/23929
; CURRENT APPLICATION NUMBER: US/11/443,428A
; CURRENT FILING DATE: 2006-05-31
; NUMBER OF SEQ ID NOS: 1034312
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 833089
; LENGTH: 194
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-443-428A-833089

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Query Match          100.0%; Score 994; DB 3; Length 194;
Best Local Similarity 100.0%;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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      |||
Db      1 MKIWTSEHVFDPHPWETVTTAAMQKYPNPMNPSVVGVDVDRHIDPSGKLHSHRLLSTEWG 60

Qy      61 LPSIVKSLIGAARTKTYVQEHSSVVDPEKTMELKSTNISFTNMVSVDERLIYKPHQDPE 120
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Db      61 LPSIVKSLIGAARTKTYVQEHSSVVDPEKTMELKSTNISFTNMVSVDERLIYKPHQDPE 120

Qy      121 KTVLTQEAIITVKGVSLSYLEGLMASTISSNASKGREAMEWVIHKLNAEIEELTASARG 180
      |||
Db      121 KTVLTQEAIITVKGVSLSYLEGLMASTISSNASKGREAMEWVIHKLNAEIEELTASARG 180

Qy      181 TIRTPMAAAFAEK 194
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Db 181 TIRTPMAAAFAEK 194

RESULT 9

US-11-443-428A-833091
 ; Sequence 833091, Application US/11443428A
 ; Patent No. 7745391
 ; GENERAL INFORMATION:
 ; APPLICANT: Mintz, Liat
 ; APPLICANT: Xie, Hangqing
 ; APPLICANT: Dahari, Dvir
 ; APPLICANT: Levanon, Erez
 ; APPLICANT: Freilich, Shiri
 ; APPLICANT: Beck, Nili
 ; APPLICANT: Zhu, Wei-Yong
 ; APPLICANT: Wasserman, Alon
 ; APPLICANT: Hermesh, Chen
 ; APPLICANT: Azar, Idit
 ; APPLICANT: Bernstein, Jeanne
 ; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
 ; FILE REFERENCE: 02/23929
 ; CURRENT APPLICATION NUMBER: US/11/443,428A
 ; CURRENT FILING DATE: 2006-05-31
 ; NUMBER OF SEQ ID NOS: 1034312
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 833091
 ; LENGTH: 194
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-11-443-428A-833091

Query Match 100.0%; Score 994; DB 3; Length 194;
 Best Local Similarity 100.0%;
 Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MKIWTSEHVFDHPWETVTTAAMQKYPNPMNPSVVGVDVDRHIDPSGKLHSHRLLSTEWG	60
Db	1	MKIWTSEHVFDHPWETVTTAAMQKYPNPMNPSVVGVDVDRHIDPSGKLHSHRLLSTEWG	60
Qy	61	LPSIVKSLIGAARTKTYVQEHSVVDPVEKTMELKSTNISFTNMVSVDERLIYKPHQDPE	120
Db	61	LPSIVKSLIGAARTKTYVQEHSVVDPVEKTMELKSTNISFTNMVSVDERLIYKPHQDPE	120
Qy	121	KTVLTQEAIIITVKGVSLSYLEGLMASTISSNASKGREAMEWVIHKLNAEIEELTASARG	180
Db	121	KTVLTQEAIIITVKGVSLSYLEGLMASTISSNASKGREAMEWVIHKLNAEIEELTASARG	180
Qy	181	TIRTPMAAAFAEK 194	
Db	181	TIRTPMAAAFAEK 194	

RESULT 10

US-11-443-428A-833093
 ; Sequence 833093, Application US/11443428A
 ; Patent No. 7745391
 ; GENERAL INFORMATION:
 ; APPLICANT: Mintz, Liat
 ; APPLICANT: Xie, Hangqing
 ; APPLICANT: Dahari, Dvir
 ; APPLICANT: Levanon, Erez
 ; APPLICANT: Freilich, Shiri
 ; APPLICANT: Beck, Nili
 ; APPLICANT: Zhu, Wei-Yong
 ; APPLICANT: Wasserman, Alon
 ; APPLICANT: Hermesh, Chen
 ; APPLICANT: Azar, Idit

```
; APPLICANT: Bernstein, Jeanne
; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
; FILE REFERENCE: 02/23929
; CURRENT APPLICATION NUMBER: US/11/443,428A
; CURRENT FILING DATE: 2006-05-31
; NUMBER OF SEQ ID NOS: 1034312
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 833093
; LENGTH: 194
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-443-428A-833093
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Query Match          100.0%; Score 994; DB 3; Length 194;
Best Local Similarity 100.0%;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 MKIWTSEHVFDPHWETVTTAAMQKYPNPMNPSVVGVDVDRHIDPSGKLHSHRLLSTEWG 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MKIWTSEHVFDPHWETVTTAAMQKYPNPMNPSVVGVDVDRHIDPSGKLHSHRLLSTEWG 60

Qy     61 LPSIVKSLIGAARTKTYVQEHSSVDPVEKTMELKSTNISFTNMVSDERLIYKPHQDPE 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 LPSIVKSLIGAARTKTYVQEHSSVDPVEKTMELKSTNISFTNMVSDERLIYKPHQDPE 120

Qy    121 KTVLTQEAIITVKGVSLSSYLEGLMASTISSNASKGREAMEWVIHKLNAEIELTASARG 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 KTVLTQEAIITVKGVSLSSYLEGLMASTISSNASKGREAMEWVIHKLNAEIELTASARG 180

Qy    181 TIRTPMAAAFAEK 194
      ||||||||||||
Db    181 TIRTPMAAAFAEK 194
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RESULT 11
US-11-443-428A-833095
; Sequence 833095, Application US/11443428A
; Patent No. 7745391
; GENERAL INFORMATION:
; APPLICANT: Mintz, Liat
; APPLICANT: Xie, Hangqing
; APPLICANT: Dahari, Dvir
; APPLICANT: Levanon, Erez
; APPLICANT: Freilich, Shiri
; APPLICANT: Beck, Nili
; APPLICANT: Zhu, Wei-Yong
; APPLICANT: Wasserman, Alon
; APPLICANT: Hermesh, Chen
; APPLICANT: Azar, Idit
; APPLICANT: Bernstein, Jeanne
; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
; FILE REFERENCE: 02/23929
; CURRENT APPLICATION NUMBER: US/11/443,428A
; CURRENT FILING DATE: 2006-05-31
; NUMBER OF SEQ ID NOS: 1034312
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 833095
; LENGTH: 194
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-443-428A-833095
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Query Match          100.0%; Score 994; DB 3; Length 194;
Best Local Similarity 100.0%;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 MKIWTSEHVFDPHWETVTTAAMQKYPNPMNPSVVGVDVDRHIDPSGKLHSHRLLSTEWG 60
```

```

Db          1 MKIWTSEHVFDHPWETVTTAAMQKYPNPMNPSVVGVDVDRHIDPSGKLHSHRLLSTEWG 60
Qy          61 LPSIVKSLIGAARTKTYVQEHSVVDPVEKTMELKSTNISFTNMVSVDERLIYKPHPQDPE 120
Db          61 LPSIVKSLIGAARTKTYVQEHSVVDPVEKTMELKSTNISFTNMVSVDERLIYKPHPQDPE 120
Qy          121 KTVLTQEAIITVKGVSLSYLEGLMASTISSNASKGREAMEWVIHKLNAEIEELTASARG 180
Db          121 KTVLTQEAIITVKGVSLSYLEGLMASTISSNASKGREAMEWVIHKLNAEIEELTASARG 180
Qy          181 TIRTPMAAAFAEK 194
Db          181 TIRTPMAAAFAEK 194

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RESULT 12

US-11-443-428A-833099

; Sequence 833099, Application US/11443428A

; Patent No. 7745391

; GENERAL INFORMATION:

; APPLICANT: Mintz, Liat

; APPLICANT: Xie, Hanqing

; APPLICANT: Dahari, Dvir

; APPLICANT: Levanon, Erez

; APPLICANT: Freilich, Shiri

; APPLICANT: Beck, Nili

; APPLICANT: Zhu, Wei-Yong

; APPLICANT: Wasserman, Alon

; APPLICANT: Hermesh, Chen

; APPLICANT: Azar, Idit

; APPLICANT: Bernstein, Jeanne

; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES

; FILE REFERENCE: 02/23929

; CURRENT APPLICATION NUMBER: US/11/443,428A

; CURRENT FILING DATE: 2006-05-31

; NUMBER OF SEQ ID NOS: 1034312

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 833099

; LENGTH: 194

; TYPE: PRT

; ORGANISM: Homo sapiens

US-11-443-428A-833099

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Query Match          100.0%; Score 994; DB 3; Length 194;
Best Local Similarity 100.0%;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MKIWTSEHVFDHPWETVTTAAMQKYPNPMNPSVVGVDVDRHIDPSGKLHSHRLLSTEWG 60
Db          1 MKIWTSEHVFDHPWETVTTAAMQKYPNPMNPSVVGVDVDRHIDPSGKLHSHRLLSTEWG 60
Qy          61 LPSIVKSLIGAARTKTYVQEHSVVDPVEKTMELKSTNISFTNMVSVDERLIYKPHPQDPE 120
Db          61 LPSIVKSLIGAARTKTYVQEHSVVDPVEKTMELKSTNISFTNMVSVDERLIYKPHPQDPE 120
Qy          121 KTVLTQEAIITVKGVSLSYLEGLMASTISSNASKGREAMEWVIHKLNAEIEELTASARG 180
Db          121 KTVLTQEAIITVKGVSLSYLEGLMASTISSNASKGREAMEWVIHKLNAEIEELTASARG 180
Qy          181 TIRTPMAAAFAEK 194
Db          181 TIRTPMAAAFAEK 194

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RESULT 13

US-11-443-428A-833098

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; Sequence 833098, Application US/11443428A
; Patent No. 7745391
; GENERAL INFORMATION:
; APPLICANT: Mintz, Liat
; APPLICANT: Xie, Hanqing
; APPLICANT: Dahari, Dvir
; APPLICANT: Levanon, Erez
; APPLICANT: Freilich, Shiri
; APPLICANT: Beck, Nili
; APPLICANT: Zhu, Wei-Yong
; APPLICANT: Wasserman, Alon
; APPLICANT: Hermesh, Chen
; APPLICANT: Azar, Idit
; APPLICANT: Bernstein, Jeanne
; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
; FILE REFERENCE: 02/23929
; CURRENT APPLICATION NUMBER: US/11/443,428A
; CURRENT FILING DATE: 2006-05-31
; NUMBER OF SEQ ID NOS: 1034312
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 833098
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-443-428A-833098
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Query Match          94.1%; Score 935; DB 3; Length 184;
Best Local Similarity 94.8%;
Matches 184; Conservative 0; Mismatches 0; Indels 10; Gaps 1;
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Qy      1 MKIWTSEHVFDHPWETVTTAAMQKYPNPMNPSVVGVDVDRHIDPSGKLHSHRLLSTEWG 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MKIWTSEHVFDHPWETVTTAAMQKYPNPMNPSVVGVDVDRHIDPSGKLHSHRLLSTEWG 60

Qy     61 LPSIVKSLIGAARTKTYVQEHSSVVDPEKTMELKSTNISFTNMVSVDERLIYKPHQDPE 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 LPSIVKSLIGAARTKTYVQEHSSVVDPEKTMELKSTNISFTNMVSVDERLIYKPHQDPE 120

Qy    121 KTVLTQEAIITVKVGSLSYLEGLMASTISSNASKGREAMEWVIHKLNAEIELTASARG 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 KTVLTQEAIITVKVGSLSYLEGLM-----GREAMEWVIHKLNAEIELTASARG 170

Qy    181 TIRTPMAAAFAEK 194
      ||||||||||||||
Db    171 TIRTPMAAAFAEK 184
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RESULT 14
US-11-443-428A-833097
; Sequence 833097, Application US/11443428A
; Patent No. 7745391
; GENERAL INFORMATION:
; APPLICANT: Mintz, Liat
; APPLICANT: Xie, Hanqing
; APPLICANT: Dahari, Dvir
; APPLICANT: Levanon, Erez
; APPLICANT: Freilich, Shiri
; APPLICANT: Beck, Nili
; APPLICANT: Zhu, Wei-Yong
; APPLICANT: Wasserman, Alon
; APPLICANT: Hermesh, Chen
; APPLICANT: Azar, Idit
; APPLICANT: Bernstein, Jeanne
; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
; FILE REFERENCE: 02/23929
; CURRENT APPLICATION NUMBER: US/11/443,428A
; CURRENT FILING DATE: 2006-05-31
```

; NUMBER OF SEQ ID NOS: 1034312
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 833097
 ; LENGTH: 179
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-11-443-428A-833097

Query Match 90.9%; Score 903.5; DB 3; Length 179;
 Best Local Similarity 92.3%;
 Matches 179; Conservative 0; Mismatches 0; Indels 15; Gaps 1;

Qy 1 MKIINTSEHVFDHPWETVTTAAMQKYPNPMNPSVVGVDVDRHIDPSGKLHSHRLLSTEWG 60
 |
 Db 1 MKIINTSEHVFDHPWETVTTAAMQKYPNPMNPSVVGVDVDRHIDPSGKLHSHRLLSTEWG 60
 |
 Qy 61 LPSIVKSLIGAARTKTYVQEHSSVVDPEKTMELKSTNISFTNMVSDERLIYKPHQPDPE 120
 |
 Db 61 LPSIVKSLIGAARTKTYVQEHSSVVDPEKTMELKSTN-----KPHQPDPE 105
 |
 Qy 121 KTVLTQEAII TVKGVSLSSYLEGLMASTISSNASKGREAMEWVIHKLNAEIELTASARG 180
 |
 Db 106 KTVLTQEAII TVKGVSLSSYLEGLMASTISSNASKGREAMEWVIHKLNAEIELTASARG 165
 |
 Qy 181 TIRTPMAAAFAEK 194
 |
 Db 166 TIRTPMAAAFAEK 179

RESULT 15

US-11-443-428A-833092

; Sequence 833092, Application US/11443428A

; Patent No. 7745391

; GENERAL INFORMATION:

; APPLICANT: Mintz, Liat

; APPLICANT: Xie, Hanqing

; APPLICANT: Dahari, Dvir

; APPLICANT: Levanon, Erez

; APPLICANT: Freilich, Shiri

; APPLICANT: Beck, Nili

; APPLICANT: Zhu, Wei-Yong

; APPLICANT: Wasserman, Alon

; APPLICANT: Hermesh, Chen

; APPLICANT: Azar, Idit

; APPLICANT: Bernstein, Jeanne

; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES

; FILE REFERENCE: 02/23929

; CURRENT APPLICATION NUMBER: US/11/443,428A

; CURRENT FILING DATE: 2006-05-31

; NUMBER OF SEQ ID NOS: 1034312

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 833092

; LENGTH: 176

; TYPE: PRT

; ORGANISM: Homo sapiens

US-11-443-428A-833092

Query Match 89.6%; Score 891; DB 3; Length 176;
 Best Local Similarity 90.2%;
 Matches 175; Conservative 1; Mismatches 0; Indels 18; Gaps 1;

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 |
 Db 1 MKIINTSEHVFDHPWETVTTAAMQKYPNPMNPSVVGVDVDRHIDPSGKLHSHRLLSTEWG 60
 |
 Qy 61 LPSIVKSLIGAARTKTYVQEHSSVVDPEKTMELKSTNISFTNMVSDERLIYKPHQPDPE 120
 |

```
Db          61 LPSIVKSLIGAARTKTYVQEHVVDPVEKTMELKSTNISFTNMVSVDERLIYKPHPQDPE 120
Qy          121 KTVLTQEAIITVKGVSLSYLEGLMASTISSNASKGREAMEWVIHKLNAEIEELTASARG 180
              :|||||
Db          121 -----NYLEGLMASTISSNASKGREAMEWVIHKLNAEIEELTASARG 162
Qy          181 TIRTPMAAAFAEK 194
              |||
Db          163 TIRTPMAAAFAEK 176
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Search completed: December 14, 2010, 11:25:12

Job time : 27.1914 secs

SCORE 3.9

SCORE Search Results Details for Application 09556178 and Search Result 20101214_103256_us-09-556-178-3.rapbm.

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This page gives you Search Results detail for the Application 09556178 and Search Result 20101214_103256_us-09-556-178-3.rapbm.

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OM protein - protein search, using sw model

Run on: December 14, 2010, 11:27:17 ; Search time 156 Seconds
(without alignments)
1680.685 Million cell updates/sec

Title: US-09-556-178-3
Perfect score: 994
Sequence: 1 MKIWTSEHVFDHPWETVTTA.....TASARGTIRTPMAAAFAEK 194

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 6210261 seqs, 1354514112 residues

Total number of hits satisfying chosen parameters: 6210261

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_Main:*

- 1: /ABSS/Data/CRF/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
- 2: /ABSS/Data/CRF/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
- 3: /ABSS/Data/CRF/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
- 4: /ABSS/Data/CRF/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
- 5: /ABSS/Data/CRF/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
- 6: /ABSS/Data/CRF/ptodata/1/pubpaa/US11A_PUBCOMB.pep:*
- 7: /ABSS/Data/CRF/ptodata/1/pubpaa/US11B_PUBCOMB.pep:*
- 8: /ABSS/Data/CRF/ptodata/1/pubpaa/US12_PUBCOMB.pep:*

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	994	100.0	194	5	US-10-917-503-13188	Sequence 13188, A
2	994	100.0	194	6	US-11-371-354-75395	Sequence 75395, A
3	994	100.0	194	6	US-11-443-428A-833084	Sequence 833084,
4	994	100.0	194	6	US-11-443-428A-833085	Sequence 833085,
5	994	100.0	194	6	US-11-443-428A-833086	Sequence 833086,
6	994	100.0	194	6	US-11-443-428A-833087	Sequence 833087,
7	994	100.0	194	6	US-11-443-428A-833088	Sequence 833088,
8	994	100.0	194	6	US-11-443-428A-833089	Sequence 833089,
9	994	100.0	194	6	US-11-443-428A-833091	Sequence 833091,

10	994	100.0	194	6	US-11-443-428A-833093	Sequence 833093,
11	994	100.0	194	6	US-11-443-428A-833095	Sequence 833095,
12	994	100.0	194	6	US-11-443-428A-833099	Sequence 833099,
13	994	100.0	194	6	US-11-582-861-8527	Sequence 8527, Ap
14	981	98.7	211	5	US-10-756-149-5549	Sequence 5549, Ap
15	981	98.7	211	5	US-10-529-348-1450	Sequence 1450, Ap
16	981	98.7	211	5	US-10-533-069-1393	Sequence 1393, Ap
17	981	98.7	211	6	US-11-582-861-8526	Sequence 8526, Ap
18	981	98.7	211	7	US-11-597-825-1144	Sequence 1144, Ap
19	981	98.7	211	8	US-12-081-546-1450	Sequence 1450, Ap
20	935	94.1	184	6	US-11-443-428A-833098	Sequence 833098,
21	903.5	90.9	179	6	US-11-443-428A-833097	Sequence 833097,
22	892	89.7	268	6	US-11-582-861-8003	Sequence 8003, Ap
23	891	89.6	176	6	US-11-443-428A-833092	Sequence 833092,
24	820	82.5	164	6	US-11-443-428A-833090	Sequence 833090,
25	653	65.7	172	4	US-10-094-749-2348	Sequence 2348, Ap
26	653	65.7	172	6	US-11-166-372-2348	Sequence 2348, Ap
27	601	60.5	207	6	US-11-443-428A-779447	Sequence 779447,
28	584	58.8	143	4	US-10-029-386-30911	Sequence 30911, A
29	524	52.7	215	6	US-11-097-143-19569	Sequence 19569, A
30	511	51.4	104	6	US-11-443-428A-833096	Sequence 833096,
31	369	37.1	136	6	US-11-443-428A-779446	Sequence 779446,
32	369	37.1	136	6	US-11-443-428A-779448	Sequence 779448,
33	263	26.5	183	5	US-10-739-930-5837	Sequence 5837, Ap
34	263	26.5	183	6	US-11-056-355B-28229	Sequence 28229, A
35	263	26.5	183	6	US-11-056-355B-31819	Sequence 31819, A
36	263	26.5	183	6	US-11-056-355B-72715	Sequence 72715, A
37	263	26.5	183	6	US-11-516-230-72824	Sequence 72824, A
38	263	26.5	183	6	US-11-713-768-28229	Sequence 28229, A
39	263	26.5	183	6	US-11-713-768-31819	Sequence 31819, A
40	263	26.5	183	6	US-11-713-768-72715	Sequence 72715, A
41	263	26.5	183	7	US-11-819-621-5837	Sequence 5837, Ap
42	263	26.5	222	6	US-11-056-355B-28228	Sequence 28228, A
43	263	26.5	222	6	US-11-056-355B-31818	Sequence 31818, A
44	263	26.5	222	6	US-11-056-355B-72714	Sequence 72714, A
45	263	26.5	222	6	US-11-713-768-28228	Sequence 28228, A

ALIGNMENTS

RESULT 1

US-10-917-503-13188

; Sequence 13188, Application US/10917503

; Publication No. US20070105122A1

; GENERAL INFORMATION:

; APPLICANT: OTA, TOSHIO

; APPLICANT: ISOGAI, TAKAO

; APPLICANT: NISHIKAWA, TETSUO

; APPLICANT: HAYASHI, KOJI

; APPLICANT: SAITO, KAORU

; APPLICANT: YAMAMOTO, JUNICHI

; APPLICANT: ISHII, SHIZUKO

; APPLICANT: SUGIYAMA, TOMOYASU

; APPLICANT: WAKAMATSU, AI

; APPLICANT: NAGAI, KEIICHI

; APPLICANT: OTSUKI, TETSUJI

; TITLE OF INVENTION: PRIMERS FOR SYNTHESIZING FULL-LENGTH cDNA AND THEIR USE

; FILE REFERENCE: 084335/0123

; CURRENT APPLICATION NUMBER: US/10/917,503

; CURRENT FILING DATE: 2004-08-13

; PRIOR APPLICATION NUMBER: US/09/629,469

; PRIOR FILING DATE: 2000-07-28

; PRIOR APPLICATION NUMBER: JP 1999-248036

; PRIOR FILING DATE: 1999-07-29

; PRIOR APPLICATION NUMBER: JP 1999-300253

; PRIOR FILING DATE: 1999-08-27

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; PRIOR APPLICATION NUMBER: JP 2000-118776
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: JP 2000-183767
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: JP 2000-241899
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/159,590
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: 60/183,322
; PRIOR FILING DATE: 2000-02-17
; NUMBER OF SEQ ID NOS: 19025
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13188
; LENGTH: 194
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-917-503-13188

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Query Match          100.0%; Score 994; DB 5; Length 194;
Best Local Similarity 100.0%;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MKIWTSEHVFDPHWETVTTAAMQKYPNPMNPSVVGVDVDRHIDPSGKLHSHRLLSTEWG 60
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Db      1 MKIWTSEHVFDPHWETVTTAAMQKYPNPMNPSVVGVDVDRHIDPSGKLHSHRLLSTEWG 60

Qy     61 LPSIVKSLIGAARTKTYVQEHSVVDPVEKTMELKSTNISFTNMVSVDERLIYKPHQPDP 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 LPSIVKSLIGAARTKTYVQEHSVVDPVEKTMELKSTNISFTNMVSVDERLIYKPHQPDP 120

Qy    121 KTVLTQEAIITVKGVSLSSYLEGLMASTISSNASKGREAMEWVIHKLNAEIEELTASARG 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 KTVLTQEAIITVKGVSLSSYLEGLMASTISSNASKGREAMEWVIHKLNAEIEELTASARG 180

Qy    181 TIRTPMAAAFAEK 194
        ||||||||||||
Db    181 TIRTPMAAAFAEK 194

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RESULT 2

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US-11-371-354-75395
; Sequence 75395, Application US/11371354
; Publication No. US20060275794A1
; GENERAL INFORMATION:
; APPLICANT: CARRINO, JOHN
; APPLICANT: LIANG, FENG
; TITLE OF INVENTION: COLLECTIONS OF MATCHED BIOLOGICAL REAGENTS AND METHODS FOR
; TITLE OF INVENTION: IDENTIFYING MATCHED REAGENTS
; FILE REFERENCE: INV-1005-UT2
; CURRENT APPLICATION NUMBER: US/11/371,354
; CURRENT FILING DATE: 2006-03-07
; PRIOR APPLICATION NUMBER: 60/673,045
; PRIOR FILING DATE: 2005-04-19
; PRIOR APPLICATION NUMBER: 60/665,199
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: 60/665,200
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: 60/659,493
; PRIOR FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: 60/659,492
; PRIOR FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: 60/953,586
; PRIOR FILING DATE: 2005-02-15
; PRIOR APPLICATION NUMBER: 60/651,390
; PRIOR FILING DATE: 2005-02-08
; NUMBER OF SEQ ID NOS: 78682
; SOFTWARE: PatentIn version 3.3

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; SEQ ID NO 75395
; LENGTH: 194
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-371-354-75395
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Query Match      100.0%; Score 994; DB 6; Length 194;
Best Local Similarity 100.0%;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 MKIWTSEHVFDPHWETVTTAAMQKYPNPMNPSVVGVDVDRHIDPSGKLHSHRLLSTEWG 60
Db      1 MKIWTSEHVFDPHWETVTTAAMQKYPNPMNPSVVGVDVDRHIDPSGKLHSHRLLSTEWG 60

Qy     61 LPSIVKSLIGAARTKTYVQEHSSVVDPEKTMELKSTNISFTNMVSDERLIYKPHQDPE 120
Db     61 LPSIVKSLIGAARTKTYVQEHSSVVDPEKTMELKSTNISFTNMVSDERLIYKPHQDPE 120

Qy    121 KTVLTQEAIITVKGVSLSSYLEGLMASTISSNASKGREAMEWVIHKLNAEIELTASARG 180
Db    121 KTVLTQEAIITVKGVSLSSYLEGLMASTISSNASKGREAMEWVIHKLNAEIELTASARG 180

Qy    181 TIRTPMAAAFAEK 194
Db    181 TIRTPMAAAFAEK 194
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RESULT 3
US-11-443-428A-833084
; Sequence 833084, Application US/11443428A
; Publication No. US20070083334A1
; GENERAL INFORMATION:
; APPLICANT: Mintz, Liat
; APPLICANT: Xie, Hangqing
; APPLICANT: Dahari, Dvir
; APPLICANT: Levanon, Erez
; APPLICANT: Freilich, Shiri
; APPLICANT: Beck, Nili
; APPLICANT: Zhu, Wei-Yong
; APPLICANT: Wasserman, Alon
; APPLICANT: Hermesh, Chen
; APPLICANT: Azar, Idit
; APPLICANT: Bernstein, Jeanne
; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
; FILE REFERENCE: 02/23929
; CURRENT APPLICATION NUMBER: US/11/443,428A
; CURRENT FILING DATE: 2006-05-31
; NUMBER OF SEQ ID NOS: 1034312
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 833084
; LENGTH: 194
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-443-428A-833084
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Query Match      100.0%; Score 994; DB 6; Length 194;
Best Local Similarity 100.0%;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 MKIWTSEHVFDPHWETVTTAAMQKYPNPMNPSVVGVDVDRHIDPSGKLHSHRLLSTEWG 60
Db      1 MKIWTSEHVFDPHWETVTTAAMQKYPNPMNPSVVGVDVDRHIDPSGKLHSHRLLSTEWG 60

Qy     61 LPSIVKSLIGAARTKTYVQEHSSVVDPEKTMELKSTNISFTNMVSDERLIYKPHQDPE 120
Db     61 LPSIVKSLIGAARTKTYVQEHSSVVDPEKTMELKSTNISFTNMVSDERLIYKPHQDPE 120
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```

Qy      121 KTVLTQEAIITVKGVSLSYLEGLMASTISSNASKGREAMEWVIHKLNAEIEELTASARG 180
        |||
Db      121 KTVLTQEAIITVKGVSLSYLEGLMASTISSNASKGREAMEWVIHKLNAEIEELTASARG 180

Qy      181 TIRTPMAAAFAEK 194
        |||
Db      181 TIRTPMAAAFAEK 194
    
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RESULT 4
US-11-443-428A-833085
; Sequence 833085, Application US/11443428A
; Publication No. US20070083334A1
; GENERAL INFORMATION:
; APPLICANT: Mintz, Liat
; APPLICANT: Xie, Hanqing
; APPLICANT: Dahari, Dvir
; APPLICANT: Levanon, Erez
; APPLICANT: Freilich, Shiri
; APPLICANT: Beck, Nili
; APPLICANT: Zhu, Wei-Yong
; APPLICANT: Wasserman, Alon
; APPLICANT: Hermesh, Chen
; APPLICANT: Azar, Idit
; APPLICANT: Bernstein, Jeanne
; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
; FILE REFERENCE: 02/23929
; CURRENT APPLICATION NUMBER: US/11/443,428A
; CURRENT FILING DATE: 2006-05-31
; NUMBER OF SEQ ID NOS: 1034312
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 833085
; LENGTH: 194
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-443-428A-833085
    
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```

Query Match          100.0%; Score 994; DB 6; Length 194;
Best Local Similarity 100.0%;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
    
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Qy      1 MKIWTSEHVDFHPWETVTTAAMQKYPNPMNPSVVGVDVLDRIHIDPSGKLHSHRLLSTEWG 60
        |||
Db      1 MKIWTSEHVDFHPWETVTTAAMQKYPNPMNPSVVGVDVLDRIHIDPSGKLHSHRLLSTEWG 60

Qy      61 LPSIVKSLIGAARTKTYVQEHSVVDPVEKTMELKSTNISFTNMVSDVERLIYKPHQPDPE 120
        |||
Db      61 LPSIVKSLIGAARTKTYVQEHSVVDPVEKTMELKSTNISFTNMVSDVERLIYKPHQPDPE 120

Qy      121 KTVLTQEAIITVKGVSLSYLEGLMASTISSNASKGREAMEWVIHKLNAEIEELTASARG 180
        |||
Db      121 KTVLTQEAIITVKGVSLSYLEGLMASTISSNASKGREAMEWVIHKLNAEIEELTASARG 180

Qy      181 TIRTPMAAAFAEK 194
        |||
Db      181 TIRTPMAAAFAEK 194
    
```

```

RESULT 5
US-11-443-428A-833086
; Sequence 833086, Application US/11443428A
; Publication No. US20070083334A1
; GENERAL INFORMATION:
; APPLICANT: Mintz, Liat
; APPLICANT: Xie, Hanqing
; APPLICANT: Dahari, Dvir
; APPLICANT: Levanon, Erez
    
```

```

; APPLICANT: Freilich, Shiri
; APPLICANT: Beck, Nili
; APPLICANT: Zhu, Wei-Yong
; APPLICANT: Wasserman, Alon
; APPLICANT: Hermesh, Chen
; APPLICANT: Azar, Idit
; APPLICANT: Bernstein, Jeanne
; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
; FILE REFERENCE: 02/23929
; CURRENT APPLICATION NUMBER: US/11/443,428A
; CURRENT FILING DATE: 2006-05-31
; NUMBER OF SEQ ID NOS: 1034312
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 833086
; LENGTH: 194
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-443-428A-833086

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Query Match          100.0%; Score 994; DB 6; Length 194;
Best Local Similarity 100.0%;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MKIWTSEHVFDPHWETVTTAAMQKYPNPMNPSVVGVDVDRHIDPSGKLHSHRLLSTEWG 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MKIWTSEHVFDPHWETVTTAAMQKYPNPMNPSVVGVDVDRHIDPSGKLHSHRLLSTEWG 60

Qy      61 LPSIVKSLIGAARTKTYVQEHSSVVDPEKTMELKSTNISFTNMVSVDERLIYKPHQDPE 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 LPSIVKSLIGAARTKTYVQEHSSVVDPEKTMELKSTNISFTNMVSVDERLIYKPHQDPE 120

Qy      121 KTVLTQEAIIITVKVGLSSYLEGLMASTISSNASKGREAMEWVIHKLNAEIELTASARG 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 KTVLTQEAIIITVKVGLSSYLEGLMASTISSNASKGREAMEWVIHKLNAEIELTASARG 180

Qy      181 TIRTPMAAAFAEK 194
        ||||||||||||
Db      181 TIRTPMAAAFAEK 194

```

RESULT 6

```

US-11-443-428A-833087
; Sequence 833087, Application US/11443428A
; Publication No. US20070083334A1
; GENERAL INFORMATION:
; APPLICANT: Mintz, Liat
; APPLICANT: Xie, Hanqing
; APPLICANT: Dahari, Dvir
; APPLICANT: Levanon, Erez
; APPLICANT: Freilich, Shiri
; APPLICANT: Beck, Nili
; APPLICANT: Zhu, Wei-Yong
; APPLICANT: Wasserman, Alon
; APPLICANT: Hermesh, Chen
; APPLICANT: Azar, Idit
; APPLICANT: Bernstein, Jeanne
; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
; FILE REFERENCE: 02/23929
; CURRENT APPLICATION NUMBER: US/11/443,428A
; CURRENT FILING DATE: 2006-05-31
; NUMBER OF SEQ ID NOS: 1034312
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 833087
; LENGTH: 194
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-443-428A-833087

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Query Match          100.0%; Score 994; DB 6; Length 194;
Best Local Similarity 100.0%;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MKIINTSEHVFDHPWETVTTAAMQKYPNPMNPSVVGVDVDRHIDPSGKLHSHRLLSTEWG 60
      |||
Db      1 MKIINTSEHVFDHPWETVTTAAMQKYPNPMNPSVVGVDVDRHIDPSGKLHSHRLLSTEWG 60

Qy     61 LPSIVKSLIGAARTKTYVQEHSVVDPVEKTMELKSTNISFTNMVSVDERLIYKPHPQDPE 120
      |||
Db     61 LPSIVKSLIGAARTKTYVQEHSVVDPVEKTMELKSTNISFTNMVSVDERLIYKPHPQDPE 120

Qy    121 KTVLTQEAIIITVKGVSLSYLEGLMASTISSNASKGREAMEWVWIKHLNAEIELTASARG 180
      |||
Db    121 KTVLTQEAIIITVKGVSLSYLEGLMASTISSNASKGREAMEWVWIKHLNAEIELTASARG 180

Qy    181 TIRTPMAAAFAEK 194
      |||
Db    181 TIRTPMAAAFAEK 194

```

RESULT 7

```

US-11-443-428A-833088
; Sequence 833088, Application US/11443428A
; Publication No. US20070083334A1
; GENERAL INFORMATION:
; APPLICANT: Mintz, Liat
; APPLICANT: Xie, Hanqing
; APPLICANT: Dahari, Dvir
; APPLICANT: Levanon, Erez
; APPLICANT: Freilich, Shiri
; APPLICANT: Beck, Nili
; APPLICANT: Zhu, Wei-Yong
; APPLICANT: Wasserman, Alon
; APPLICANT: Hermesh, Chen
; APPLICANT: Azar, Idit
; APPLICANT: Bernstein, Jeanne
; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
; FILE REFERENCE: 02/23929
; CURRENT APPLICATION NUMBER: US/11/443,428A
; CURRENT FILING DATE: 2006-05-31
; NUMBER OF SEQ ID NOS: 1034312
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 833088
; LENGTH: 194
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-443-428A-833088

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Query Match          100.0%; Score 994; DB 6; Length 194;
Best Local Similarity 100.0%;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MKIINTSEHVFDHPWETVTTAAMQKYPNPMNPSVVGVDVDRHIDPSGKLHSHRLLSTEWG 60
      |||
Db      1 MKIINTSEHVFDHPWETVTTAAMQKYPNPMNPSVVGVDVDRHIDPSGKLHSHRLLSTEWG 60

Qy     61 LPSIVKSLIGAARTKTYVQEHSVVDPVEKTMELKSTNISFTNMVSVDERLIYKPHPQDPE 120
      |||
Db     61 LPSIVKSLIGAARTKTYVQEHSVVDPVEKTMELKSTNISFTNMVSVDERLIYKPHPQDPE 120

Qy    121 KTVLTQEAIIITVKGVSLSYLEGLMASTISSNASKGREAMEWVWIKHLNAEIELTASARG 180
      |||
Db    121 KTVLTQEAIIITVKGVSLSYLEGLMASTISSNASKGREAMEWVWIKHLNAEIELTASARG 180

Qy    181 TIRTPMAAAFAEK 194

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Db 181 TIRTPMAAAFAEK 194

RESULT 8

US-11-443-428A-833089
 ; Sequence 833089, Application US/11443428A
 ; Publication No. US20070083334A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Mintz, Liat
 ; APPLICANT: Xie, Hangqing
 ; APPLICANT: Dahari, Dvir
 ; APPLICANT: Levanon, Erez
 ; APPLICANT: Freilich, Shiri
 ; APPLICANT: Beck, Nili
 ; APPLICANT: Zhu, Wei-Yong
 ; APPLICANT: Wasserman, Alon
 ; APPLICANT: Hermesh, Chen
 ; APPLICANT: Azar, Idit
 ; APPLICANT: Bernstein, Jeanne
 ; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
 ; FILE REFERENCE: 02/23929
 ; CURRENT APPLICATION NUMBER: US/11/443,428A
 ; CURRENT FILING DATE: 2006-05-31
 ; NUMBER OF SEQ ID NOS: 1034312
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 833089
 ; LENGTH: 194
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-11-443-428A-833089

Query Match 100.0%; Score 994; DB 6; Length 194;
 Best Local Similarity 100.0%;
 Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MKIINTSEHVFDPHPWETVTTAAMQKYPNPMNPSVVGVDVDRHIDPSGKLHSHRLLSTEWG	60
Db	1	MKIINTSEHVFDPHPWETVTTAAMQKYPNPMNPSVVGVDVDRHIDPSGKLHSHRLLSTEWG	60
Qy	61	LPSIVKSLIGAARTKTYVQEHSSVDPVEKTMELKSTNISFTNMVSDERLIYKPHQDPDE	120
Db	61	LPSIVKSLIGAARTKTYVQEHSSVDPVEKTMELKSTNISFTNMVSDERLIYKPHQDPDE	120
Qy	121	KTVLTQEAIITVKGVSLSSYLEGLMASTISSNASKGREAMEWVIHKLNAEIEELTASARG	180
Db	121	KTVLTQEAIITVKGVSLSSYLEGLMASTISSNASKGREAMEWVIHKLNAEIEELTASARG	180
Qy	181	TIRTPMAAAFAEK 194	
Db	181	TIRTPMAAAFAEK 194	

RESULT 9

US-11-443-428A-833091
 ; Sequence 833091, Application US/11443428A
 ; Publication No. US20070083334A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Mintz, Liat
 ; APPLICANT: Xie, Hangqing
 ; APPLICANT: Dahari, Dvir
 ; APPLICANT: Levanon, Erez
 ; APPLICANT: Freilich, Shiri
 ; APPLICANT: Beck, Nili
 ; APPLICANT: Zhu, Wei-Yong
 ; APPLICANT: Wasserman, Alon
 ; APPLICANT: Hermesh, Chen


```

; APPLICANT: Azar, Idit
; APPLICANT: Bernstein, Jeanne
; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
; FILE REFERENCE: 02/23929
; CURRENT APPLICATION NUMBER: US/11/443,428A
; CURRENT FILING DATE: 2006-05-31
; NUMBER OF SEQ ID NOS: 1034312
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 833091
; LENGTH: 194
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-443-428A-833091

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```

Query Match          100.0%; Score 994; DB 6; Length 194;
Best Local Similarity 100.0%;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MKIWTSEHVFDPHWETVTTAAMQKYPNPMNPSVVGVDVLDLRHIDPSGKLHSHRLLSTEWG 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MKIWTSEHVFDPHWETVTTAAMQKYPNPMNPSVVGVDVLDLRHIDPSGKLHSHRLLSTEWG 60

Qy     61 LPSIVKSLIGAARTKTYVQEHSVVDPVEKTMELKSTNISFTNMVSDERLIYKPHQDPE 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 LPSIVKSLIGAARTKTYVQEHSVVDPVEKTMELKSTNISFTNMVSDERLIYKPHQDPE 120

Qy    121 KTVLTQEAIITVKGVSLSSYLEGLMASTISSNASKGREAMEWVIHKLNAEIEELTASARG 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 KTVLTQEAIITVKGVSLSSYLEGLMASTISSNASKGREAMEWVIHKLNAEIEELTASARG 180

Qy    181 TIRTPMAAAFAEK 194
      ||||||||||||
Db    181 TIRTPMAAAFAEK 194

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RESULT 10

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US-11-443-428A-833093
; Sequence 833093, Application US/11443428A
; Publication No. US20070083334A1
; GENERAL INFORMATION:
; APPLICANT: Mintz, Liat
; APPLICANT: Xie, Hanqing
; APPLICANT: Dahari, Dvir
; APPLICANT: Levanon, Erez
; APPLICANT: Freilich, Shiri
; APPLICANT: Beck, Nili
; APPLICANT: Zhu, Wei-Yong
; APPLICANT: Wasserman, Alon
; APPLICANT: Hermesh, Chen
; APPLICANT: Azar, Idit
; APPLICANT: Bernstein, Jeanne
; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
; FILE REFERENCE: 02/23929
; CURRENT APPLICATION NUMBER: US/11/443,428A
; CURRENT FILING DATE: 2006-05-31
; NUMBER OF SEQ ID NOS: 1034312
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 833093
; LENGTH: 194
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-443-428A-833093

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```

Query Match          100.0%; Score 994; DB 6; Length 194;
Best Local Similarity 100.0%;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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US-11-443-428A-833095
; Sequence 833095, Application US/11443428A
; Publication No. US20070083334A1
; GENERAL INFORMATION:
; APPLICANT: Mintz, Liat
; APPLICANT: Xie, Hanqing
; APPLICANT: Dahari, Dvir
; APPLICANT: Levanon, Erez
; APPLICANT: Freilich, Shiri
; APPLICANT: Beck, Nili
; APPLICANT: Zhu, Wei-Yong
; APPLICANT: Wasserman, Alon
; APPLICANT: Hermesh, Chen
; APPLICANT: Azar, Idit
; APPLICANT: Bernstein, Jeanne
; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
; FILE REFERENCE: 02/23929
; CURRENT APPLICATION NUMBER: US/11/443,428A
; CURRENT FILING DATE: 2006-05-31
; NUMBER OF SEQ ID NOS: 1034312
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 833095
; LENGTH: 194
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-443-428A-833095

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Query Match 100.0%; Score 994; DB 6; Length 194;
Best Local Similarity 100.0%;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MKIINTSEHVFDPHWETVTTAAMQKYPNPMPNSVVGVDVDRHIDPSGKLHSHRLLSTEWG	60
Db	1	MKIINTSEHVFDPHWETVTTAAMQKYPNPMPNSVVGVDVDRHIDPSGKLHSHRLLSTEWG	60
Qy	61	LPSIVKSLIGAARTKTYVQEHSVVDPVEKTMELKSTNISFTNMVSVDERLIYKHPQDPE	120
Db	61	LPSIVKSLIGAARTKTYVQEHSVVDPVEKTMELKSTNISFTNMVSVDERLIYKHPQDPE	120
Qy	121	KTVLTQEAIIIVKGVSLSYSLEGLMASTISSNASKGREAMEWVIHKLNAEIEELTASARG	180
Db	121	KTVLTQEAIIIVKGVSLSYSLEGLMASTISSNASKGREAMEWVIHKLNAEIEELTASARG	180
Qy	181	TIRTPMAAAFAEK	194
Db	181	TIRTPMAAAFAEK	194

<http://es.ScoreAccessWeb/GetItem.action?AppId=09556178&seqId=09323b6780fb2282&ItemName=2010...> 1/10/11

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US-11-443-428A-833099
; Sequence 833099, Application US/11443428A
; Publication No. US20070083334A1
; GENERAL INFORMATION:
; APPLICANT: Mintz, Liat
; APPLICANT: Xie, Hangqing
; APPLICANT: Dahari, Dvir
; APPLICANT: Levanon, Erez
; APPLICANT: Freilich, Shiri
; APPLICANT: Beck, Nili
; APPLICANT: Zhu, Wei-Yong
; APPLICANT: Wasserman, Alon
; APPLICANT: Hermesh, Chen
; APPLICANT: Azar, Idit
; APPLICANT: Bernstein, Jeanne
; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
; FILE REFERENCE: 02/23929
; CURRENT APPLICATION NUMBER: US/11/443,428A
; CURRENT FILING DATE: 2006-05-31
; NUMBER OF SEQ ID NOS: 1034312
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 833099
; LENGTH: 194
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-443-428A-833099
    
```

```

Query Match          100.0%; Score 994; DB 6; Length 194;
Best Local Similarity 100.0%;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
    
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Qy      1 MKIINTSEHVDFHPWETVTTAAMQKYPNPMNPSVVGVDVDRHIDPSGKLHSHRLLSTEWG 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MKIINTSEHVDFHPWETVTTAAMQKYPNPMNPSVVGVDVDRHIDPSGKLHSHRLLSTEWG 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy      61 LPSIVKSLIGAARTKTYVQEHSSVVDPEKTMELKSTNISFTNMVSDERLIYKPHQDPE 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 LPSIVKSLIGAARTKTYVQEHSSVVDPEKTMELKSTNISFTNMVSDERLIYKPHQDPE 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy      121 KTVLTQEAIITVKGVSLSYLEGLMASTISSNASKGREAMEWVIHKLNAEIELTASARG 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 KTVLTQEAIITVKGVSLSYLEGLMASTISSNASKGREAMEWVIHKLNAEIELTASARG 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy      181 TIRTPMAAAFAEK 194
        ||||||||||||
Db      181 TIRTPMAAAFAEK 194
    
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RESULT 13
US-11-582-861-8527
; Sequence 8527, Application US/11582861
; Publication No. US20070099251A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Hui
; APPLICANT: Aebersold, Rudolf H.
; TITLE OF INVENTION: TISSUE- AND SERUM-DERIVED GLYCOPROTEINS
; TITLE OF INVENTION: AND METHODS OF THEIR USE
; FILE REFERENCE: 460092.404
; CURRENT APPLICATION NUMBER: US/11/582,861
; CURRENT FILING DATE: 2006-10-17
; PRIOR APPLICATION NUMBER: US 60/728,044
; PRIOR FILING DATE: 2005-10-17
; NUMBER OF SEQ ID NOS: 14918
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8527
; LENGTH: 194
; TYPE: PRT
    
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; ORGANISM: Homo sapiens
US-11-582-861-8527

Query Match 100.0%; Score 994; DB 6; Length 194;
Best Local Similarity 100.0%;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MKIWTSEHVFDHPWETVTTAAMQKYPNPMNPSVVGVDVDRHIDPSGKLHSHRLLSTEWG 60
      |||
Db      1 MKIWTSEHVFDHPWETVTTAAMQKYPNPMNPSVVGVDVDRHIDPSGKLHSHRLLSTEWG 60

Qy     61 LPSIVKSLIGAARTKTYVQEHSSVVDPEKTMELKSTNISFTNMVSVDERLIYKPHPQDPE 120
      |||
Db     61 LPSIVKSLIGAARTKTYVQEHSSVVDPEKTMELKSTNISFTNMVSVDERLIYKPHPQDPE 120

Qy    121 KTVLTQEAIIITVKGVSLSYLEGLMASTISSNASKGREAMEWVIHKLNAEIEELTASARG 180
      |||
Db    121 KTVLTQEAIIITVKGVSLSYLEGLMASTISSNASKGREAMEWVIHKLNAEIEELTASARG 180

Qy    181 TIRTPMAAAFAEK 194
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Db    181 TIRTPMAAAFAEK 194
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RESULT 14

US-10-756-149-5549

; Sequence 5549, Application US/10756149

; Publication No. US20050181375A1

; GENERAL INFORMATION:

; APPLICANT: Aziz, Natasha

; APPLICANT: Zlotnik, Albert

; TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS AND

; TITLE OF INVENTION: METHODS OF SCREENING FOR MODULATORS OF METASTATIC CANCER

; FILE REFERENCE: file

; CURRENT APPLICATION NUMBER: US/10/756,149

; CURRENT FILING DATE: 2004-01-12

; NUMBER OF SEQ ID NOS: 5818

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 5549

; LENGTH: 211

; TYPE: PRT

; ORGANISM: Homo Sapiens

US-10-756-149-5549

Query Match 98.7%; Score 981; DB 5; Length 211;
Best Local Similarity 98.5%;
Matches 191; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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Qy      1 MKIWTSEHVFDHPWETVTTAAMQKYPNPMNPSVVGVDVDRHIDPSGKLHSHRLLSTEWG 60
      |||
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Qy     61 LPSIVKSLIGAARTKTYVQEHSSVVDPEKTMELKSTNISFTNMVSVDERLIYKPHPQDPE 120
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Db     61 LPSIVKSLIGAARTKTYVQEHSSVVDPEKTMELKSTNISFTNMVSVDERLIYKPHPQDPE 120

Qy    121 KTVLTQEAIIITVKGVSLSYLEGLMASTISSNASKGREAMEWVIHKLNAEIEELTASARG 180
      |||
Db    121 KTVLTQEAIIITVKGVSLSYLEGLMASTISSNASKGREAMEWVIHKLNAEIEELTASARG 180

Qy    181 TIRTPMAAAFAEK 194
      |||
Db    181 TIRTPMAAAFCRE 194
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RESULT 15

US-10-529-348-1450

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; Sequence 1450, Application US/10529348
; Publication No. US20070042945A1
; GENERAL INFORMATION:
; APPLICANT: Bodary-Winter, Sarah
; APPLICANT: Clark, Hilary
; APPLICANT: Jackman, Janet
; APPLICANT: Schoenfeld, Jill
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Wu, Thomas D.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR THE TREATMENT OF PSORIASIS
; FILE REFERENCE: P1987R1-US
; CURRENT APPLICATION NUMBER: US/10/529,348
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: PCT/US03/030907
; PRIOR FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: US 60/414,006
; PRIOR FILING DATE: 2002-09-25
; NUMBER OF SEQ ID NOS: 2484
; SEQ ID NO 1450
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-529-348-1450
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Query Match          98.7%;  Score 981;  DB 5;  Length 211;
Best Local Similarity 98.5%;
Matches 191;  Conservative 1;  Mismatches 2;  Indels 0;  Gaps 0;
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      |||||||
Db      1 MKIWTSEHVFDPHWETVTTAAMQKYPNPMNPSVVGVDVDRHIDPSGKLHSHRLLSTEWG 60

Qy     61 LPSIVKSLIGAARTKTYVQEHSVVDPVEKTMELKSTNISFTNMVSVDERLIYKPHPQDPE 120
      |||||||
Db     61 LPSIVKSLIGAARTKTYVQEHSVVDPVEKTMELKSTNISFTNMVSVDERLIYKPHPQDPE 120

Qy    121 KTVLTQEAIITVKGVSLSSYLEGLMASTISSNASKGREAMEWVIHKLNAEIEELTASARG 180
      |||||||
Db    121 KTVLTQEAIITVKGVSLSSYLEGLMASTISSNASKGREAMEWVIHKLNAEIEELTASARG 180

Qy    181 TIRTPMAAAFAEK 194
      |||||
Db    181 TIRTPMAAAFCRE 194
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Search completed: December 14, 2010, 11:32:16
Job time : 156.35 secs

SCORE 3.0

SCORE Search Results Details for Application 09556178 and Search Result 20101214_103257_us-09-556-178-3.rapbn.

[Score Home Page](#) [Retrieve Application List](#) [SCORE System Overview](#) [SCORE FAQ](#) [Comments / Suggestions](#)

This page gives you Search Results detail for the Application 09556178 and Search Result 20101214_103257_us-09-556-178-3.rapbn.

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OM protein - protein search, using sw model

Run on: December 14, 2010, 11:32:21 ; Search time 1 Seconds
(without alignments)
1087.643 Million cell updates/sec

Title: US-09-556-178-3
Perfect score: 994
Sequence: 1 MKINTSEHVFDPHWETVTTA.....TASARGIIRTPMAAAAFAEK 194

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 23285 seqs, 2931653 residues

Total number of hits satisfying chosen parameters: 23285

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_New:*
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3: /ABSS/Data/CRF/ptodata/2/pubpaa/US12_NEW_PUB.pep:*
SUMMARIES

Result No.	% Query						Description
	Score	Match Length	DB	ID			
1	80.5	8.1	448	3	US-12-803-125-22		Sequence 22, Appl
2	75.5	7.6	449	2	US-11-919-265-66		Sequence 66, Appl
3	75.5	7.6	468	3	US-12-441-246B-209		Sequence 209, App
4	72	7.2	456	2	US-11-919-265-68		Sequence 68, Appl
5	71.5	7.2	451	3	US-12-803-125-20		Sequence 20, Appl
6	71.5	7.2	456	2	US-11-919-265-30		Sequence 30, Appl
7	70	7.0	452	3	US-12-739-480-26		Sequence 26, Appl
8	70	7.0	467	3	US-12-740-815-41		Sequence 41, Appl
9	70	7.0	471	3	US-12-441-246B-45		Sequence 45, Appl
10	70	7.0	471	3	US-12-441-246B-159		Sequence 159, App
11	70	7.0	471	3	US-12-739-480-38		Sequence 38, Appl
12	69	6.9	452	3	US-12-739-480-27		Sequence 27, Appl
13	69	6.9	452	3	US-12-739-480-28		Sequence 28, Appl
14	69	6.9	452	3	US-12-739-480-29		Sequence 29, Appl
15	69	6.9	452	3	US-12-739-480-30		Sequence 30, Appl
16	69	6.9	471	3	US-12-441-246B-81		Sequence 81, Appl
17	69	6.9	471	3	US-12-441-246B-87		Sequence 87, Appl
18	69	6.9	471	3	US-12-441-246B-117		Sequence 117, App
19	69	6.9	471	3	US-12-441-246B-123		Sequence 123, App
20	69	6.9	471	3	US-12-441-246B-129		Sequence 129, App
21	69	6.9	471	3	US-12-441-246B-135		Sequence 135, App
22	69	6.9	471	3	US-12-441-246B-141		Sequence 141, App
23	69	6.9	471	3	US-12-441-246B-171		Sequence 171, App
24	69	6.9	471	3	US-12-441-246B-177		Sequence 177, App

25	69	6.9	471	3	US-12-441-246B-183	Sequence 183, App
26	69	6.9	471	3	US-12-441-246B-189	Sequence 189, App
27	69	6.9	471	3	US-12-441-246B-241	Sequence 241, App
28	69	6.9	471	3	US-12-739-480-39	Sequence 39, Appl
29	69	6.9	471	3	US-12-739-480-40	Sequence 40, Appl
30	69	6.9	471	3	US-12-739-480-41	Sequence 41, Appl
31	69	6.9	471	3	US-12-739-480-42	Sequence 42, Appl
32	69	6.9	471	3	US-12-739-480-49	Sequence 49, Appl
33	69	6.9	475	3	US-12-740-815-61	Sequence 61, Appl
34	68.5	6.9	453	2	US-11-919-265-32	Sequence 32, Appl
35	68.5	6.9	455	3	US-12-787-588-52	Sequence 52, Appl
36	68.5	6.9	577	3	US-12-787-588-66	Sequence 66, Appl
37	68.5	6.9	578	3	US-12-787-588-74	Sequence 74, Appl
38	68	6.8	471	3	US-12-441-246B-99	Sequence 99, Appl
39	68	6.8	471	3	US-12-441-246B-153	Sequence 153, App
40	67.5	6.8	452	3	US-12-720-483A-73	Sequence 73, Appl
41	67.5	6.8	470	3	US-12-800-989-2	Sequence 2, Appli
42	67.5	6.8	716	3	US-12-800-989-3	Sequence 3, Appli
43	67	6.7	471	3	US-12-441-246B-147	Sequence 147, App
44	67	6.7	471	3	US-12-441-246B-165	Sequence 165, App
45	67	6.7	1160	3	US-12-717-789A-118	Sequence 118, App

ALIGNMENTS

RESULT 1

US-12-803-125-22

; Sequence 22, Application US/12803125

; Publication No. US20100297153A1

; GENERAL INFORMATION:

; APPLICANT: Crucell Holland B.V.

; APPLICANT: Geuijen, Cecilia A.W.

; APPLICANT: de Kruif, Cornelis A.

; TITLE OF INVENTION: Binding molecules for treatment and detection of cancer

; FILE REFERENCE: 0113 EP P00 PRI

; CURRENT APPLICATION NUMBER: US/12/803,125

; CURRENT FILING DATE: 2010-06-18

; PRIOR APPLICATION NUMBER: US/11/665,102

; PRIOR FILING DATE: 2007-04-10

; NUMBER OF SEQ ID NOS: 67

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 22

; LENGTH: 448

; TYPE: PRI

; ORGANISM: Artificial sequence

; FEATURE:

; OTHER INFORMATION: Heavy chain CR2361

US-12-803-125-22

Query Match 8.1%; Score 80.5; DB 3; Length 448;

Best Local Similarity 22.5%;

Matches 57; Conservative 34; Mismatches 87; Indels 75; Gaps 13;

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Qy      4 WISEHVFDFHWETVI-----TAAMQKYPN-----PMNPS-----VVGVDVLDRHIDP--- 45
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Db      99 WAPSHSFYD-WGQGTLVTVSASTIKGFSVFPLAPSSKSTSGGTAALGCLVKDYFPEFVTV 157

Qy      46 ---SGKLHS---HRL-----LSTEWGLPSIVKSLIGAARTKY---VQHSVVDVPEKTE 92
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      158 SWNSGALTSVGHITFPVAVLQSSGLYSLSSVTVVPSSSLGTQTYICNVNHPKPNNTKVKDRVE 217

Qy      93 LKSTNISFT-----NMVSVDERLIYKHPHQD-----PEKTLTQEAIIITVKGVSL 138
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      218 FKSCDKHTICPPCPAPPELLGGFSVFLFPPKPKDILMISRTFEVTVGVVDSHEDPEVKFN 277

Qy      139 SYLEGLMASTISSNASKGREA-----MEWVIHK-----LNAEIE 172
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      278 WYVDGV---EVHNAKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE 334

Qy      173 ELTASARGITIRP 185
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Db      335 KTISKAKGQFPREP 347

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